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50 AGCCTCATTTCCCTTTTATGCCTCCTTCTCTGTTCATGTTCTTCATGGTTGCCC---- 103
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Best Local Similarity:
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Sequence 23909, A
Sequence 5559, Ap
Sequence 7685, Ap
Sequence 1258, Ap
Sequence 108, Ap
Sequence 1012, A
Sequence 23596, A
Sequence 23596, A
Sequence 23596, A
Sequence 23596, A
                                                                                           (without alignments)
2325.347 Million cell updates/sec
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                                                                           2, 2006, 05:24:40; Search time 11.1 Seconds
GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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1: /cgn2 6/prodata/1/iaa/5 COMB.pep:*
2: /cgn2 6/prodata/1/iaa/6 COMB.pep:*
3: /cgn2 6/prodata/1/iaa/H_COMB.pep:*
4: /cgn2 6/prodata/1/iaa/H_COMB.pep:*
5: /cgn2 6/prodata/1/iaa/RE COMB.pep:*
6: /cgn2 6/prodata/1/iaa/RE COMB.pep:*
                                                  - protein search, using frame_plus_n2p model
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US-09-252-991A-23909
US-09-328-355-5559
US-09-328-352-5559
US-09-328-352-7685
US-09-538-092-1258
US-09-52-991A-21920
US-09-252-991A-2359
US-09-252-991A-33596
US-09-252-991A-23598
US-09-252-991A-23598
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Maximum Match 100%
Listing first 45 summaries
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Sequence 2405, Application US/09540236

Patent No. 6673910
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2405
LENGTH: 543
   16789, A 212789, A 422789, A 522789, A 5227800, A 52278
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US-09-288-523A-90

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US-09-288-991A-10597

US-09-282-991A-20186

US-09-902-540-16463

US-09-252-991A-26099

US-09-252-991A-18427

US-09-252-991A-18427

US-09-252-991A-19739

US-09-252-991A-317125

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US-09-252-991A-31715

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US-09-252-991A-31716
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; TYPE: PRT
; ORGANISM: M.catarrhalis
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1229 ACCGCOAGCTCCTAAACACACACACACACACACACACACACACACA	ORGANISH: FKH   ORGANISH:   Organish:
143 TCCAAACCTGTCCTCCTGGACAACATCGTG	Db 289 ArgGlmlametGlmasnSerThilleglyGlmaspleuLeualaGlmGlmValProbhe 308  878 CaGaGCGCCCAACCGGCTGATCAGCGCAAAAGGACTCGACGGCGCCC 937  879 PheTrpThrGlulleAspLeulleAlaAspAsnVallleLysLeuAsnGlyHisSerAsp 328  879 PheTrpThrGlulleAspLeulleAlaAspAsnVallleLysLeuAsnGlyHisSerAsp 328  879 GCCAACCGCGATTGCGGGGGGGCTCAAGACGCCCGAAAAAGGGTC 997  870 Sille Caractagagagagagagagagagagagagagagagagagaga

Qy         1208 GCCACAAAAGACAAAGGCCTGACCGCAGCTCGTAACCAGCCTGCATGCCAAAACC 1264           Db         441 LeuSerGlyAlaProTrpArgLeuHisGlySerSerSerAlaSerLeuHisSerLysAla 460           Qy         1265 TTCATTGTGGACGCAACGCATCTTCATCGGCTCATTCAACCTCGACCCCGTTCCGCA 1324           Si:	Oy 1442 AACCGCCTGCAATGGCACGATCCCGCCACCCGAAAAACCTACCCG 1486	MО	NS-09-328-352-5559   Alignment Scores:   3.59e-31   Length:   271   271   271   272   272   272   273   273   273   273   273   274   274   275   27	Oy 104 CCACTGGAAGACGGAAGCCGTCATTCAATACTTCCAAACCTGTCCTGGAC 163
88	431 CTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCTACGCAA 487	599 GACGAATACTTCAAAGTCGGTGAGGACACCGTTTTCGCCGACCTCGACATCCTCGCCACC 658  [	821 GAAACCGTCGAACAGTCGCCCCTTCTACCAAAAATACAGACGGACGC 868	1028 AAATCCGGCACACACACTGGCAAAACTGGTGCAGGACGCATACACGTTACCGTCTG 1087
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Sequence 7685, Application US/09328352
Sequence 7685, Application US/09328352
Patent No. 5652958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: 1999-66-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7685
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                                        1106 ACCGACGTTGCCGCCGTCCATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCC 1165
                                                                                            GGCATCAAACTCTACGAGCTGCAACCC-----------AACCAT 1198
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62
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                                                                                                                                                                1199 GCCGTCCCCGCCACAAAGACAAA---GGCCTGACCGGCAGCTCCGTAACCAGCCTGCAT
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Best Local Similarity:
Query Match:
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US-09-328-352-7685
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ORGANISM:
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Batent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT BILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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| 17 PheAsnProTyrArgPheArgLysTyrArgAlaMetAspMetIleLeuAspLeuLysArg
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                                                                                                            CGCGGGTTGGACGATCTCCTGCTCGCCCTCGACAGCCCATCCCAATATCGAAGTGCGCCTG
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-328-352-5591
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61.9%
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US-09-328-352-5591
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LENGTH: 275
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1287 rThrProThr----SerSerTh 1293
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1267 rPheThrThrIleThrLeuProThrThrProThrSerPheThrThrThrThrThrTh
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FRATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q02817
US-09-538-092-1288
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|LeuArgllePheAspTyrLeuPheArgPheLysLysValAsnHisArgMetHisAsnLys 179
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SerTyrLeuLysGluLeuLeuGluHisAsnProlleGlnTrpSer-----LysAlaHis 295
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Sequence 1258, Application US/09538092

Sequence 1258, Application US/09538092

Sequence 1258, Application US/09538092

Sequence 1258, Application US/09538092

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 1596-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

LENGTH: 5179
                                              s::||| |||||| :::||||::: serArglleTyrLeulleArgAsnAlaLysGluThrIleAspLeuGlnTyrTyrIleTrp
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; FILE REFERENCE: 107196.136 ; CURRENT APPLICATION NUMBER: US/09/252,991A ; CURRENT FILING DATE: 1999-02-18 ; PRIOR PILING DATE: 1998-02-18 ; PRIOR PILING DATE: 1998-02-18 ; PRIOR PILING DATE: 1998-07-27 ; NUMBER OF SEQ ID NOS: 33142 ; SEQ ID NO 21920 ; LENGTH: 822 ; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa iix-09-25-991A-21920	Alignment Scores: Pred. No.: Score: Score: Score: Bercent Similarity: Destruct Similarity: 11.4* Matches: Matches: 195 Wery Match: 11.4* Matches: 11.4* Matches: 195 Weight: 11.4* Matches: 195 Mismatches: 106 Match: 11.4* Matches: 107 Match: 11.4* Matches: 108 Match	103 AGGINATOR TO CONTINUATE TO	205 ATCCGACATCTACCTGCTCGACG ::     ::  21 AlaTyrArgTrpArgAlaGlyGl 265 CGAATCTGCCGAACACAGCCTCG	Oy 325 CAGGGTI	Qy         409GTTGGACGATCCTCGCTCGACAGCCATCC	Oy 463GTTCAACCCCTTCGTCCTACGCAAATGGCGCGCACTCGGCTACCTCAACCGA 513	274 ArgargAspArgGlnGlnArgArgGlnProAlaArgProArgProGlnArgGlnHisAla 541
Oy 696GCTACTGGGCAAGCCATTCGGCCACGGCATCATCGGCAGGGC 748	Oy 863 GGACGCATCGACAGGCGTCCAAACCGGCTGATCAGCGACACCCTGCAAAAGGA 922	1563 iProproprothrithrithrithrithrithrithrithrithrithri	Db 1593 rThrThrProProProThrThrProSerProFroThrThrThrThrThrThrThrThrFroPr 1613  Qy 1143	Oy 1238 TCCGTAACCAGCCTGCAAAACCTTCATTGTGGACGCAAAACGCTTCATCGTCGC 1297	1418 TACCGCGTTACCTCGACAACACACACCGCGCGCACGATGGCACGGTCCCGCCACCGAAAA  1708 011eThrThrThrThrThrProSerSerThrThrThrThrProSerSerCCGCCGCAACACCGAAACCCGAAACCCGAAACCCGAAACCCGAAACGCCACCGAAACGCCACCGAAAAATCCTATCATC	DD 1725 OINTINIMETINITINITIONSELFIOININITINITINITININININININININININININ	RESULT 7 US-09-252-991A-21920 ; Sequence 21920, Application US/09252991A ; Sequence 21920, Application US/09252991A ; Patent No. 655195 ; GENERAL INFORMATION: ; APPLICANT: Marc J. Rubenfield et al. ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

	Dy 737 AspGlnGlnTrpArgProValLeuArgSerGlyA  Oy 1501 CAAACTTTGGAAACGCATCGCCGCAAAAATCCTA  Db 757 GlnCysGlnHisAlaHisArgGlnArgArgHisP  RESULT 8  US-09-487-558B-108  Sequence 108, Application US/09487558B  Sequence 108, Application US/09487558B  APPLICANT: Busby, Robert  APPLICANT: Hecht, Peter  APPLICANT: Hecht, Peter  APPLICANT: Holtzman, Doug  APPLICANT: Mandden, Kevin  APPLICANT: Mandden, Kevin  APPLICANT: Manden, Mary  APPLICANT: Moley Jodd  APPLICANT: Sleama, Sofie  APPLICANT: Sleama, Sofie  APPLICANT: Sherman, Amir  APPLICANT: Sleama, Jeff  APPLICANT: Sleama, Sofie  APPLICANT: Sleama, Sofie	; TITLE REFERENCE: 109272.130 ; CURRENT APPLICATION NUMBER: US/09/487,558B ; CURRENT FILING DATE: 2000-01-19 ; PRIOR PPLICATION NUMBER: US 60/487,558 ; PRIOR PRILING DATE: 1999-10-20 ; NUMBER OF SEQ ID NOS: 446 ; SCOTWARE: PATENTIN VERSION 3.0 ; SEQ ID NO 108 ; LENGTH: 1367 ; TYPE: PRT ; TYPE: PRT ; ORGANISM: Saccharomyces cerevisiae US-09-487-558B-108 Alignment Scores: 2.52e-17 Hatches: Score: 323.50 Percent Similarity: 40.7% Matches: Percent Similarity: 25.4% Mismatches Ouery Match: 25.4% Mismatches Ouery Match: 25.4% Mismatches Ouery Match: 25.4% Mismatches Ouery Match: 21.13% Indels: BB: US-10-665-990A-13 (1-1561) x US-09-487-558B-108  Qy RGTTCATGTTCTTCATGGTTGCCCCACTG
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|ArgileProGluGlnGlyAlaAspPro 736
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|AspProGlyArgArgArgHisGly 756
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કે જ	CGTGCGCGTACGCCTGCTGTTGGACGACAACAACGCGGGGGTTGGACGATCTCCTGCT	OY 1225 CCTGACCGGCAGCTCCGTAACCAGCCTGCAAAACCTTCATTGTGGACGCAAACG 1284
ර් සි		OY 1285 CATCTTCATCGGCTCATTCAACCTCGACCCCGTTCCGCACGGCTCAATACCGAATGGG 1344
<i>₹</i> 6	CTTCGTCCTACGCAATGGCGCGCACTCGGCTACCTGACCGACTTCCCCGCCT	Oy 1345 CGTCGTCATCGAAAGCCCCAAAATCGCAGACGGACCGCACCCTCGCCGATACCAC 1404
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\ \dot \d	ACGCAATATCGGCGACGAATACTTCAAAGTCGGTGAGGACACCGTTTTCGCCGACCGTGGA	Oy 1423CGTTACCCTCGACAAACACAACGCCTGCAATGGCACGA 1461
2 70	646 CATCCTCGCCACCGCCACCGCCGCGAGGTATCGCACGACGTTCGACCTACTGGGC 705	Qy         1462 TCCCGCCACCCGAAAAACCTACCCGAACGAACCCGAAGCCAAACTTTGGAAACGCATCGC 1521
6 상 18	288 ArgArgGlnArgArgGluValArgArgGlnProLeuSerArgGlnThrAlaGly 305 706 AAGCCATTCCGC	1522 CGCAAAAATCCTATCCCTGCTGCCCATCGA 1551
QQ	::: 306 ArgAlaArgArgProAlaProAlaAspArgArgAlaGlyTrpGlnGlyProGlyArg 325	Db 606 ArgArgAlaGlyGlyArgArgLeuProAlaValHisArg 618
oy Dp	727 CACGCGCATCGTCGCGCGCGACGACGTCGGCAAGGGTCTTCAAGCACTCGGATACAACGA 786	
	787 CGAAACATCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGCCCCTCTA 846	; GENERAL INFORMATION: ; APPLICANT: MATC J. RUbenfield et al. ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ; TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
<u>ک</u> خ		
	CCTGATCAGCGACACCCCTGCAAAAGGACTCGACCG	
	PIOASPAIGNISAIGUINFIOAIGAIGFREAFGFIOAIGAIGFIOVALGIULEUGIYGIY CGACCGCCGCAAACCGCCGATTGCCGGGAGGCTGCAAAGACGC	; NUMBER OF SEQ ID NOS: 33142 ; SEQ ID NO 23696 ; LENGTH: 618 ; TYPE: PRT
	397 ArgProGluProAlaAlaAspGluArgGluGluGluArgArgArgArgAlaValLeuGlyArg 416 973	; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-23696
	ď	6 Length: Matches:
	CCCTATTTCGTCCCTACAAATCCGGCACAGACGCACTGGC 1          rgArgAlaArgProGlyGlyAlaArgGlnArgArgArgGly 4	ercent Similarity: 34.8% est Local Similarity: 29.0% uery Match: 2
	10	
3	45/AlakroAlaGlyArgArgGLy1yIDeUkrOGlUkrOGlyGlAAlaGln1yrArgABD 4/5	Qy 169 CCTGCAAATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACGA 228

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US-09-252-991A-16789

Sequence 16789, Application US/09252991A

Sequence 16789, Application US/09252991A

Sequence 16789, Application US/09252991A

Sequence 16789, Application US/09252991A

GENERAL INFORMATION:

TITLE OF INVERTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVERTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT FILING DATE: 1099-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                  CATCGGCTCATICAACCTCGACCCCCGTTCCGCACGGCTCAATACCGAAATGGCCGTCGT 1350
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                                                                                           -GCTGCTCAAAGCCGGCATCAA 1173
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----AlaThrGlyGlnProGlyGlnArgArg 273
                                                        ArgalaHisProProTyrArgGlnArgHisLeuArgProGlyPheArgAlaGlyAspPro 293
                                                                                                                           294 ArgArgArgArgThrAspHisGlnTrpProAlaGlyHisProArgGlnArgMetAspGln 313
                                                                                                                                                                                                                                                                                                             ---ArgleuGluGlnArgArgProAlaGlyGlnArgArgClnLeuAlaThrArgAlaGlu 367
                                                                                                                                                                                                                                                                                                                                                                               368 ArgargleuproTrpGlnArgProArgHis-----GlnProArgArgLeuArgProGlu 385
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                               CGTTGCCGCCGTCCATTCCGGCTACGTCAAATA-------
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Matches:
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---ArgPro-
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|110 LeuAlaGluAla---GlyHiSArgAlaValArgGlnGlnArgArgArgHisProGlyAla 128
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                                                                                                                                                                       196 CAACGGGCTATCCGACATCTACCTGCTCGACGACCCCCACGAAGCCCTTGCCGCCCG--- 252
                                                                                                                                                                                                                                     253 ---CGCCGCCCTTATCGAATCTGCCGAACACAGCCTCGATTTGCAATACTACATTTGGCG 309
                                                                                                                                                                                                                                                                                                    CAACGACATITCCGGCAGGCTGCTCTTCAACCICATGIA---CCTTGCCGCAGAACGCGG 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 Gly---ArgArgGlnProHisArgHisArgArgLeuArgGln-------ProGly 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  769 AGCACTCGGATACAACGACGAAACATCCAGACACGCGCTCCTGCGCTACCGCGAAACCGT 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATTCCGCCCACACGCCACGCGCATCATCCGCAGCGGCAACATCGGCAAGGGTCTTCA
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Matches:
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qa XX	91 ProproAlaLeuGlyGlyArgGlnHisArgHisArgArgArgProGlnGlyProArgArg 110 259CCTTATCGAATCTGCCGAACACAGCCTCGATTTGCAATA 297	1060
Dp	Pro	458 ArgArgHisArgGlyArgArgClnArgArg.
oy Oy	298	OY 1120 CGTCCATTCCGGCTACGTCAAATACCGAAAACCGCTV
ું ફ	GTTCAACCTCATGTACCTTGCCGCAGAACGGGGGGGGGG	OY 1171 CAAACTCTACGAGCTGCAACCATGCCGTCCCCGCCACAAA
à	388	1231 CGGCAGCTCCGTAACCAGCCTGCATGCCAAAACCTTCATTG
Db		Db 514 GluGlyGlyLysArgProAlaThrGlnAlaLeuGly(
රු සි	418 TCTCCTGCCTCGCCTCGACGCCATATCGAAGTGCGCCTGTTCAACCCCTTCGT 477 :::	
λ̈		Oy 1351 CATCGAAAGCCCCAAAATCGCAGAACAGATGGAGGCGCACCTCGCC
go :6	ProGluArgLeuArgGlnLeuGlnArgGlyThrAlaGlyHisArgHisLeuProProGly	1408
g S	526 CAACGGCCGCAIGCA	Db 557 ProGlyArgLeuArgLeuHisHisHeuHisArgGlnLeuArgPro
οy	28	Qy 1459 CGATCCCGCCACCGAAAAACCTACCGGAACCGAAGCCAAA
Db	246 LeuProArgHisProGlyArgHisArgLeuProHisHisHisAspGlnArgProArgArg 265	TO DESCRIPTION OF THE PROPERTY
ري م	586 ACGCAATATCGCGACGAATACTTCAAAGTCGGTGAGGACACCGTTTTCGCCGACCT 642	OY 1519 GCCCCAMANATICAL 1553 
} &		RESULT 14 US-09-134-001C-4273
qq		; Sequence 4273, Application US/09134001C ; Patent No. 6380370
ò	691 CGACCGCTACTGGGCAAGCCATTCCGCCACGCCACGCGCACGCGCATCCTCCGCAGGGGCAA 750	; GENERAL INFORMATION: ; APPLICANT: Lynn Doucette-Stamm et al ; TITLE OF INVENTION: NUCLEEC ACTD AND AMINO ACTD SEQUENCE.
qa ,		; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THEE; FILE REFERENCE: GTC-007
ර සි	751 CATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAACATCCAGACACGGCTCCT 810 320 GluGlyArgGlyGlyGluIleArgArgAlbeuArgArgArgProGlyArgProAlaPro 339	CURRENT APPLICATION NUMBER: US/09/134,001C ; CURRENT FILING DATE: 1999-08-18 ; PRIOR APPLICATION NUMBER: US 60/064,964
ò		; PRIOR FILING DATE: 1997-11-08 ; PRIOR APPLICATION NUMBER: US 60/055,779
qq	340 GlyGlyProArgHisHisArgGlnHisGlyProGlyIleArgArgHisLeuArgLeuLeu 359	; PRIOR FILING DATE: 1997-08-14 ; NUMBER OF SEQ ID NOS: 5674 ; CEO ID NO 4373
٥٠ م	841	SEQ AD 42/3   ENGTH: 49/8   TYPE: PRT
1 8		US-09-134-001C-4273
. d	GlyArgGlyLeuGlnGlnGlyThrGlyProValAlaArgGluGlyProArgAla	ent Scores: 8.84e-15 Length:
<i>λ</i> ο 7	895 CCTGATCAGCGACACCCCTGCAAAAGGACTCGACGGCGACGGCGCAAACC 945	Score: 289.50 Matches: 105 Percent Similarity: 33.2% Conservative: 68 Best Local Similarity: 23.2% Mismacches: 151
qq	400 GlyValHisArgHisProAlaProGlyHisGlyArgSerArgGlyGlnProGlyArgThr 419	10.2% Indels: 2 Gaps:

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CES RELATING TO STAPHYLOCOCCUE HERAPEUTICS
AAAAGCGTCTATCTGGT 1005
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rgGlnArgLeuGlnArg 437
                                                   -- ACTGGCAAAACTGGT 1059
                                                                                                        GCGACCGACGTTGCCGC 1119
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----ArgArgAspArg 473
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roProAlaGlnArgGly 457
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rgArgProAlaGlyGlu 513
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-------LysGluSerIleTyrIle 348
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204 AspieulystysPheArgGlniysGlyGlyHisAlaGluSerPheProSerLysLeu 223
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                                191 CATAACAACGGGCTA-------TCCGACATCTACCTGCTCGACGACCCCCAC 235
                                                     :::|||||||
122 TyrAsnAsnAlaAlaPheLeuThrThrAspAsnAspLeuThrIleTyrThrAspGlyHis 141
                                                                                                  236 GAAGCCCTTGCCGCCCCCCCCTTATCGAATCTGCCGAACACAGCCTCGATTTGCAA 295
                                                                                                                               296 TACTACATTTGGCGCAACGACATTTCCGGCAGGCTGCTGTTCAACCTCATGTACCTTGCC 355
                                                                                                                                                                                                                                           356 GCAGAACGCGGCGTGCGCGTACGCCTGCTGTTGGACGACAACAACACGCGCGGGGTTGGAC 415
                                                                                                                                                                                                                                                                                                              416 GATCTCCTGCTCGCCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTC 475
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282 LeuGlnLeuArgPhelleLeuAspTrpAsnSerGlnSerThrArgAspAsnLeuThrTyr 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   773 CTCGGATACAACGACGAAACATCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAA 832
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369 GlyGlyValAspValAsnIleMetValProAsnLysArg-----AspHisProPheVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 GlyTyrLeuLysMetileSerSerAla-----
                                                                                                                                                                                              476 GTCCTACGCAAATGGCGCGCACTCGGCTACCTGACCGAC-----TTCCCCC-----
US-10-665-990A-13 (1-1561) x US-09-134-001C-4273 (1-495)
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qa	387	TyrTrpAlaThrLeuLysAsnValAlaSerLeuLeuGluAlaGlyValAsnValTyrHis 406	
ò	1184	CTGCAACCCAACCATGCCGTCCCCGCCACAAAGACAAAGGCCTGACCGGCAGCTCCGTA 1243	m
q	407	Tyr411	
ò	1244	ACCAGCCTGCATGCCAAAACCTTCATTGTGGACGGCAAACGCATCTTCATCGGCTCATTC 1303	m
q	412	:::	
Oy B	1304	AACCTCGACCCCGTTCCGCACGGCTCAATACCGAAATGGGCGTCGTCATCGAAAGCCCC 1363    :::                       :::   AsnMetAspAsnArgSerPheThrLeuAsnPheGluValAsnAlaPheIleTyrAspGlu 449	m
ò	1364	AAAATCGCAGAAACAGATGGAGCGCACCCTCGCCGAT	σ,
ą d	450	:::     GlyValAlaArgSerLeuLysGlnAlaPheIleAsnAspMetLysLeuSerAsnLysLeu 469	
ò		ACCACACCGGAATACGCCTACCGCGTTACCCTCGACAA 14	
qq	470	ThrserGluciuTyrAlaLysArgAsnLeuLeuValLys 482	
RE US	SULT 15 - 09-252-991 Sadenece 21 Satent No. 21 GENERAL INF APPLICANT: TITLE OF II TITLE OF II TITLE OF II FILE REFERI CURRENT PPI PRIOR FILII PRIOR FILII PRIOR FILII NUMBER OF 252-9911 TYPE: PROGRAMISM:	RESULT 15 US-09-252-991A-21881 ; Sequence 21881, Application US/09252991A ; Sequence 21881, Application US/09252991A ; Sequence 21881, Application US/09252991A ; Patent No. 651795 ; GENERAL INFORMATION: ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMON; ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ; TITLE OF INVENTION: ABSCAUGE 10796-136 ; CURRENT PILING DATE: 1999-02-18 ; PRIOR APPLICATION NUMBER: US 60/074,788 ; PRIOR APPLICATION NUMBER: US 60/094,190 ; PRIOR FILING DATE: 1998-07-27 ; NUMBER OF SEQ ID NOS: 33142 ; SEQ ID NO 21881 ; LENGTH: 720 ; TYPE: PRT ; ORGANISM: PSEudomonas aeruginosa US-09-252-991A-21881	ромор
7	1000		
AI SC Pe Ou	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	es: 1.02e-14 Length: 720 289.50 Matches: 160 rity: 34.1\$ Conservative: 41 ilarity: 27.2\$ Mismatches: 209 10.2\$ Indels: 30	
ns	US-10-665-990	-990A-13 (1-1561) x US-09-252-991A-21881 (1-720)	
ò		AGAACGGACGGAAQCCGTCATTCAATACTTCCAAACCTGTCCTGGACAACATCCT	
d G	179	ArgAlaThrGlyGlnProArgArgGlnGlyHisArgArgGlnArgProAlaProHisArg 198	
oy B	172	GCADATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACGACCC 231 	
ò	, 232	CCACGAAGCCCTTGCCGCCCCCCGCGCCCCTTATCGAATCTGCCGAACACAGCCTCGATTT 291	
qq	216	GluProGlyArgArgArg 221	
õ	, 292	GCAATACTACATTTGGCGCAACGACATTTCCGGCAGGCTGCTGTTCAACCTCATGTACCT 351	
අු	222	ThrValGlnArgArgArgArgSerAlaArgGlnProGluGlnPro 236	
ò	352		
g G	237	GluargGluProArgArgArgAlaGlyGlnPro 247	

NAS

Qy         1222 AGGCCTGAC	Qy         1369 GGCAGAACAGATGGAGCGCACCCTCGCCGATACCACCCGGAATACGCCTACCGCGTTAC 1428           Db         641 ArgArgProGlyGlnProGlyTrp 648           Qy         1429 CCTCGACAAACACAACCGCCTGCAATGGCACGATCCCGCCACCCGAAAAACCTACCC 1485           Db         649 ProAspGlnCysSerArgProAlaGluHisArgAlaAlaGluArgProArgGlnProPro 668           Qy         1486 GAACGAACCCGAAGCCAAACTTGGAAACGCATGGCGCAAA 1527           Db         669 GlyArgArgArgAspheGlnProAlaGlyLeuArgAlaAlaGlyGlnAlaHisArgGlnArg 688           Qy         1528 AATCCTATCCTGCTGCCATGGAAG 1554	Db 689ProAlaGlyAlaHisHisGlnArg 696  RESULT 16 US-09-252-991A-23080 ; Sequence 23080, Application US/09252991A ; Sequence 23080, Application US/09252991A ; Patent No. 6551795 ; GENERAL INFORMATION:	PRIOR APPLICATION NUMBER: US 60/094,190   PRIOR FILING DATE: 1998-07-27   NUMBER OF SEQ ID NOS: 33142   SEQ ID NO 23080   LENGTH: 561   TYPE: PRT   ORGANISM: Pseudomonas aeruginosa   US-09-252-991A-23080   1.22e-14   Length: 561   Pred. No.: 288.00   Matches: 141   Score: 288.00   Matches: 141   Percent Similarity: 37.9\$   Conservative: 47   Best Local Similarity: 28.4\$   Mismatches: 140   DB: 2   Gaps: 30	US-10-665-990A-13 (1-1561) x US-09-252-991A-23080 (1-561)  QY 355 CGCAGAACGCGGCGTACGCCTGCTGTTGGACGACAACAACACGCGGGGGTT 411
Qy 412 GGACGATCTCCTGGCCGCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCC 471	526 CAACCG	368 ProArgProAlaArgArgArgProGlyGlnArgAsnArgArcGGCTA  368 ProArgProAlaArgArgArgArgProGlyGlnArgAsnArgArgArcGGCTA  700CTGGGCAAGCGATTCCGCCCACAAGGCTACAT  388 TrpArgHisAlaGlyGlnProArgArgProAspArgHisAlaArgArgArgArgAlaAla  739CGCAGCGGCAACATCGGCAAGGCTCTTCAAGCACTCGGATACAACGACGAACATC  739CCGCAGCGCAACATCGGCAAGGCTCTTCAAGCACTCGGATACAACGACGAACACTC  1	448 AspProAlaHisArgProGlyProGlyGlnGlnProGlyArgGlyAspLeuArgArgArg 467  bb 448 AspProAlaHisArgProGlyProGlyGlnGlnProGlyArgGlyAspLeuArgArgArg 467  cy 868CATCGACTGGCAGAGCGTCCAAACCCGCCTGATCGCGGACACCCCTGCAA 918  bb 468 ArgProGlyHisArgGlyArgSerProGlyGlnGlnArgGlnGlyHisProGlyGln 486  cy 919 AGGACTCGACCGCGCAAACCGCCGAATGCCGGGAGGCTGCAAGACGCGCTCAA 978  cy 919 AGGACTCGACCGCCGCAAACCGCCGAAACCGCGCAAAGACGCGCTCAA 978  cy 919 AGGCCCGAAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCCTACAAAAAGAGAGGGTGAAAAAGGGTCTATCTGGTTTCACCCTATTTCGTCCTACAAAAAAGGGT 1038  cy 919 AGACCCGAAAAACGGTCTATCTGGTTTCACCCTATTTCGTCCTACAAAAATGGCA 1038  cy 919 AGACCCAAAAAAAGGTCTATCTGGTTTCACCCTATTTCGTCCTACAAAAATGGTA 1166  cy 919 AGACCCACTGGCAAAACTGGTACAAGAACTGGTAAAACTGGCCAAAAAAGGTTTCAAAAACTGTCCTACAAAAATGGTAAAACTGGCAAAACTGGCAAAACTGGCAAAACTGGCAAAACTGGCAAAACTGGCAAAACTGGCAAAACTGCAAAACTGCAAAAAACTGCAAAAACTGCAAAAAAAA	516 ArgleuProGlyGlnGlpArgGlnGlyProAlaLeuArgGlnArgArgProGluArgArg 1069 CATAGACGTTAC

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NO ACID SEQUENCES RELATING TO PSEUDOMONAS OSTICS AND THERAPEUTICS
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||AaAspArgGluAlaProAlaProValAla 30
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PSEUDOMONAS

ć		Qy 1232 GGCAGCTCCGTAACCAGC
ò		Db 410
qq	144 GlnValLeuLysAsp	OV 1292 ATCGGCTCATTCAACCTCC
ζ	272 GCCGAACACAGCCTCGATTTGCAATACTACATTTGGCGCAACGACATTTCCGGCAGGCTG 331	424
qa	152 AlalysGluTyrIleHisLeuGluTyrTyrThrPheAlaLeuAspGlyLeuGlyLysArg 171	
λ	332 CTGTTCAACCTCATGTACCTTGCCGCAGAACGCGGGGGTGCGCGTACGCCTGCTGTTGGAC 391	4
QQ	::: ::: :::	444
ò	392 GACAACAACACGCGGGGTTGGACGATCTCCTGGTCGCCCTCGACAGCCATCCCAATATC 451	7141
qa	:::::: 192 AspValGlySerLys	455
δλ	3CGCCTGTTCAACCCCTTCGTCCTACGCAAAT	OY 1472 CGAAAAACCIACCCGAAC
qa	::::: 199 LysMetAlaAsnPheAspHisPheLysSerLeuGlyGlyGluVal 213	404
ò	503TACCTGACCGACTTCCCCCGCCTCAACCGCCGCATGCAC 541	:::
qq	214 GlualaPhePheAlaSerLysLeuProLeuLeuAsnPheArgMetAsnAsnAsnArgAsnHis 233	100 VALUEL
δ	542 AACAAATCCTTTACCGCGGCAAACCGCGCCACCATACTCGGCGGACGCAATATCGGCGAC 601	US-09-828-523A-90
qq	 234 ArgLysIleIleValIleAspGlyGlnLeuGlyTyrValGlyGlyPheAsnIleGlyAsp 253	; Sequence 50, Application US/US/ ; Patent No. 6764823
δλ	TTTCAAAGTCGGTGAGGACACCGTTTTCGCCGGACCTGGACA	APPLICANT: The Pharmacia & Up
qq	 254 GluTyrLeuGlyLeuGlyLysLeuGlyTyrTrpArgAspThrHisLeuArglleGlnGly 273	; FILE OF INVENTION: ANITHICACO
λΌ	662 AGCGTCGTCGCGAAGTATCGCACGACTTCGACCGCTACTGGGCATTCCGCCCAC 721	; CURRENT APPLICATION NUMBER: U ; CURRENT FILING DATE: 2001-04
qq		; PRIOR APPLICATION NUMBER: 60/ ; PRIOR FILING DATE: 2000-04-06
δλ	722 AACGCCACGCGCATCATCCGCAGCGGCAACATCGGCAAG 760	0
qq	293 ArgProGlnPheGluTyrAspValLysTyrPheProLysLysAsnGlyProLeuGly 311	; JEC 10 30 ; LENGTH: 502 ; TVDE: DDT
ò	761 GGTCTTCAAGCACTCGGATACAACGACGAACATCCAGACACGCGCTCCTGCGGTACCGC 820	
qq	311 311	
ò	821 GAAACCGTCGAACAGTCGCCCCTCTACCAAAAATACAGACGGACG	US-09-828-523A-90
qu	312AsnSerProlleGlnIleAlaAserGlyProAlaSerAspTrpHis 327	Alignment Scores:
ò	881 AGCGTCCAAACCCGCCTGATCAGCGACACCCCTGCAAAAGGACTCGACCGC 931	Score: 24-11-11-11-11-11-11-11-11-11-11-11-11-11
qq	328 GlnileGluTyrGlyTyrThrLysMetIleMetSerAla340	Fercent Similarity: 20.23 Best Local Similarity: 21.18
ò	932 GACCGCCGCAAACCGCCGATTGCCGGGAGGCTGCAAGACGCGCTCAAACAAGACAGCCCGAAAAA 991	
qq	341LysLys 342	US-10-665-990A-13 (1-1561) x US-
ò	992 AGGGTCTATCTGGTTTCACCCTATTTCGTCCTACAAAATCCGGCACAGACGCACTGGCA 1051	Qy 110 GAAGAACGGAAAGC
qq		Db 105 AspAsnLysGlnValGln
ò	1052 AAACTGGTGCAGGACGCATAGACGTTACCGTCCTGACCAACTCGCTACAGGCGACCGAC	Qy 164AACATC
qq	363 IleAlaAlaKsSerGlyValAspValHisLeuMetIleProCysLysProAsp 380	Db 125 GlyPheLeuThrGluAsn
δ	1112 GTTGCCGCCGTCCATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCATC 1171	Qy 212 ATCTACCTGCTCGACGAC
Ωp	381 HisProLeuValTyrTrpAlaThrPheSerAsnAlaSerAspLeuLeuSerSerGlyVal 400	Db 145 GlnValLeuLysAsp
δλ	1172 AAACTCTACGAGCTGCAACCAACCATGCCGTCCCCGCCACAAAAGACAAAAGCCTGACC 1231	Qy 272 GCCGAACACAGCCTCGAT
qq	401 LyslleTyr 409	Db 153 AlaLysGluTyrIleHis

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:id sequence encoded by S. aureus coding region cloned for on in E. coli.
                                              CCTGCATGCCAAAACCTTCATTGTGGACGCAAACGCATCTTC 1291
                                                                                                                                               CCTCGACAAACAACCGCCTGCAATGGCACGATCCCGCCACC 1471
                                                                                             CGCAGAACAGATGGAGCGCACCCTCGCCGATACCACCCCGAA 1411
                -::|||:::|||
-IleHisSerLysMetCysLeulleAspAspGlulleValSer 423
                                                                                                                          -----Arg 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCAAATCCGGCACACCCTCATAACAACGGGCTATCCGAC 211
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OBIAL METHODS AND MATERIALS
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uAlaLysAspLeu------
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Matches:
Conservative:
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Sequence 1597, Application US/09252991A

Sequence 17597, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Warc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PALLING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 611
                                              1412 TACGCCTACCGCGTTACCCTCGACAACACACGCCTGCAATGGCACGATCCCGCCACC 1471
                                                                                                       CGAAAAACCTACCCGAACGAACCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATC 1531
                     -----Arg 455
                                                                                                                          168 TCCTGCAAATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACG 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 Cys-----AlaArgSerSerArgProSerProAlaSerAlaArgTrpArgAlaAlaAla 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGGCTTGGACGATCTCCTGCTCGCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGT 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 TGGAAGAACGGACGGAAAGCCGTCATTTCAATACTTCCAAACCTGTCCTCCTGGACAACA
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Matches:
Conservative:
Mismatches:
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    Gaps:
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71 ArgProSerArg------
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36.6%
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490 ValSer 491
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Best Local Similarity:
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US-09-252-991A-17597
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Pred. No.:
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                 173 IleLeuHisAlaLeuGluGluLySLeuLySGlnGlyLeuGluValLySIleLeuTyrAsp 192
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LysileTyr------ThrTyrGluAsnGlyPhe--- 410
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ND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
DIAGNOSTICS AND THERAPEUTICS
TCGA-----CAAACACACCGCCTGCAATGGCACG 1460
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bArgGlyLeuAlaGlySerAlaProAlaMetSerAr 484
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Sequence 615, Application US/09976594
Sequence 615, Application US/09976594
Retent No. 6673549
GENERAL INFORMATION:
APPLICANT: FURNESS, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A L:
FILE REFRENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SEQ ID NO 615
              1526 AAAATCCTATCCCTGCTG 1543
                                411 ArgAlaLeuSerLeuLeu 416
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37.7%
26.0%
9.6%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
                                                                           RESULT 23
US-09-976-594-615
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                                                          145 AlapheLysProPheSerLeuSer-----ArgGlyLeuArgHisLeuLeu-----
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; OTHER INFORMATION: Incyte ID No. 6673549 2789525CD1
US-09-976-594-615
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6551795

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: AERUCISC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUCISCOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE REFERENCE: 107195,136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-07-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
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-----ArgLeuArgHisHisProProGlyAlaLeuLeuProGlyThrAspAlaLeuArg 382
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Matches:
Conservative:
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US-09-252-991A-29427
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ThrArgLysSerArgValSerValSerProGlyArgThrSerGlyLysValThrLysHis 442
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-----ThrargargLeuSerProSerAlaSerProProArgArgArgArgProSer 402
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483 ArgGlnTyrArgArgGlnAsnGlnGlnSerSerSerSerGlySerSerSerSer 502
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543 ArgGlyArgArgArgSerProSer--------ProProProThrArg 556
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212 AlaGlyGluArgGlnAlaProSerArgAspArgGlnHisGlnCysGlnArgArgAlaAla
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||duargLeuHisArgGlyArgProGlyTyr-----HisProAlaArgArgHis---
                                                                                                                     -----CCTGCAATGGCACGATCCCGCCACGAAAAACCTACCC
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US-09-252-991A-25018
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1171   CAAACTCTACGAGCTGCAACC	Db 669 ArgCysHisLeuPheArgThrAlaGlyAspArgCsGAATGCGGAAGCCCCAA 1365	RESULT 26 US-09-252-991A-26099 US-09-252-991A-26099 Sequence 26099, Application US/09252991A Fatent No. 6551795 GENERAL INFORMATION: FAPLICANT: Marc J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOWN TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 10796.136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 FRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 26099 LENGTH: 863 TYPE: RRT COGRANISM: PSeeudomonas aeruginosa US-09-252-991A-26099	Alignment Scores:  Pred. No.:  Scores:  Scores:  Pred. No.:  Scores:  Scores:  Pred. No.:  Scores:  Pred. No.:  Scores:  Pred. No.:  Scores:  Pred. No.:  Scores:  Pred. No.:  3.95e-13  Mismatches:  36  Mismatches:  26  Mismatches:  27  Gaps:  33  US-10-665-990A-13 (1-1561) x US-09-252-991A-26099 (1-863)  Qy  208 CGACATCTACCTGCTCGACGACCCCCCACGAAGCCCTTATCGA 267
260 AlaValArgleuGlyArgHisArgArgGlyAspGlnArgHisProGlnValGly 277  421 CCTGCTCGCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCT 480  [	574		10.21   CCLINCARANICCOCCACACACACACACACCACCACCACCACCACCACCAC
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	RESULT 27 US-09-252-991A-18427 Sequence 18427, Application US/09252991A Sequence 18427, Application US/09252991A Sequence 18427, Application US/09252991A Sequence 18427, Application US/09252991A Sequence 18427, Application US/09252991A Sequence 18427, Application US/09252991A TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUT TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUT FILE REFERENCE: 107196.136 CURRENT PELLING DATE: 1999-02-18 PRIOR PILING DATE: 1999-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 SEQ ID NO 18427 SEQ ID NO 18427 SEQ ID NO 18427
65   STUTECCGGAACACACCCT	311 CysHisArgGlyProProLeuArgArgGlyArgArgSerArgLeuProAlaAlaAspArg 330 823 AAC
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RELATING TO PSEUDOMONAS UTICS ---AGGCCTGAC 1230 ||||||| |IleArgProArg 543 CGAATACGCCTA 1419 ||| || ||| ArgargargGly 612 TGCCGCCGT--- 1122 |||||| |AspArgArgAla 508 CAAACTCTACGA 1182 ||| || || || ---ThrArgArg 523 :CGAAATGGGCGT 1347 :::|||||| AlaAspGlyArg 573 ACCCGAAGCCAA 1503 ||| ::: |GlnArgGlnGlu 650 CAAACGCATCTT 1290 1095 .----- 1110 ----- 1374 SCAATGGCA--- 1458 MaLeuProGly 448 rgArgArgGly 468 ProGlyArgPro 488 ProThrAlaAla 593 AlaGlyAlaGly 630 rgProGlnPro 428 --GlyHisPro 553 AGG 1554 ||| Arg 667

; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-18427	961 GCTGCAAGACGCGCTCAAACAGCCCGAAAAAAGCGTCTATCTGGTTTCACCCTATTTCGT
Alignment Scores: Pred. No.: Score: 269.50 Matches: 149 Score: 3.3\$ Conservative: 42 Best Local Similarity: 26.0\$ Mismatches: 190 Query Match: 2 Gaps: 29	1021 CCCTACAAAATCCGGCACAGACGCACTGGCAAAACTGGT 10
US-10-665-990A-13 (1-1561) x US-09-252-991A-18427 (1-748)	318 SerGlyLeuHisProArgProArgLeuTrpArgProGlyAlaAspGlu
OY 148 ACCTGTCCTGGACAACATCCTGGAAATCGGGCACACCCTCATAACAACGGGCT 204	Oy 1111 CGTTGCCGCTTCCATTCCGGCTACGTCAAAACCGAAAACCGCTGCTCAAAGCCGGCAT 1170 
E = E	Oy 1171 CAAACTCTACGAGCTGCAACCCAA
	Qy 1195CCATGCCGCCCCCCCCCCACAAAGACAAAGGCCT 1227 
TGCCGCAGAACGCGGCGT	Oy 1228 GACCGGCAGCTCCGTAACCAGCCTGCATGCCAAAACCTTCATTGTGGA 1275
370 GCGCGTACGCCTGCTGTTGGACGACAACAACAACGCGCGGGGTTGGACGATCTCCT 4	Qy 1276 CGGCAAACGCATCTTCATCGG
134 FIOGINAIGPFOGLIVHISPIOGLIVGIUHISGINGINHISGINATGATGGLYSEFSEFPRO 424 GCTCGCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTAACCCCTTGTTCAAC	Qy 1309 CGACCCCGTTCCGCACGGCTCAATACCGAAATGGGCGTCGTCATCGAAAGCCCCAAAAT 1368
DD 154 ThrGin	Qy 1369 CGCAGAACAGATGGAGCGCACCCTCGCGATACCACACCGGATACGCTACCGGGT 1425
544 CAAATCCTTTACCGCGACAACCGCGCCACCATACTGGGGGAGCAATATGGG	Qy 1425 1425 Db 474 LeualaSerArgAlaArgLeuLeuArgLysProLeuAlaLeuProAlaAlaLeuAlaGln 493
598GACGAATACTTCAAAGTCGGTGAGACACCGTTTTCGCCGACCTGGACATCCTCGC	Qy 1426 TACCCTCGACAACACACCCCTGCAATGGCACGATCC 1464
OD 184 GIYALAARGLEUGINAKGPROAKGILEGIYAEDALATNIVALAKGARGHIEALAPKOVAL 203 QY 655 CACCGGCAGCGTCGGCGAAGTATCGCACGACTTCGACCGCTACTGGGCAAGCCATTC 714 Dh 200 Highweli	Qy 1465CGCCACCCGAAAAACCTACCGGAACGAACCCGAAGCCAAACTTTGGAA 1512                 Db 514 AlaGlyAspargGlyAlaProArgProGluProTyrArgProArgArgPro 530
715 CGCCCACAACGC	Qy 1513 ACGCATCGCCGCAAAAATCCTACCTGCCGATCGA 1551
742CAGGGGCAACATCGGCAAGGGTCTTCAAGGACTCGGATACAA :::   ::    :     231 AlaValArgArgArgArgArgArgGlyAspGlnArgGlyAlaGluGluAlaPheArg	RESULT 28 US-09-252-991A-19467 ; Sequence 19467, Application US/09252991A ; Patent No. 6551795.
	; GENERAL INFORMATION: ; APPLICANT: Marc J. Rubenfield et al. ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
Qy 844 CTACCAAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCGCCTGAT 900	; CURRENT FILING DATE: 1999-02-18 ; CURRENT FILING DATE: 1999-02-18 ; PRIOR APPLICATION NUMBER: US 60/074,788 ; PRIOR FILING DATE: 1998-02-18
Qy 901 CAGGACACCCTGCAAAAGACTCGACCGCGACCGCGAAACGGCGGTTGCCGGGAG 960 	APPLICATION NUME FILING DATE: 19 R OF SEQ ID NOS:

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Pseudomonas aeruginosa
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204 GlyArgAlaTyrArgAlaProArgThrGlyPhe------ArgGluAlaArgThrGly
                                                                                                                                                                                                                                                                              ------SerArgAlaProGlyArgGlyAlaGlyArgGlyIleHis------
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SerLeuTyrGlyPheGlnSerIleAlaAlaProGlyAlaLeu--
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                                                                                                 Matches:
Conservative:
Mismatches:
Indels:
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                                  ORGANISM: Pseudomonas aeruginosa
                                                                                 3.76e-13
269.00
33.6%
27.2%
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                                               US-09-252-991A-19467
SEQ ID NO 19467
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Sequence 24941

Sequence 24941

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Sequence 24941

Sequence 2491

Application US/09252991A

Sequence 2491

Sequence 2491

Batent No. 6551795

GENERAL INFORMATION:

APPLICANT:

Marc J. Rubenfield et al.

APPLICANT:

APPLICANT:

TITLE OF INVENTION:

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TITLE OF INVENTION:

ABRUORA APPLICATION NUMBER:

SEQ ID NOS:

PRIOR FILING DATE:

PRIOR PILING DATE:

PRIOR PILING DATE:

PRIOR PILING DATE:

SEQ ID NOS:

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AlabroGlyProProArgGlnProAspGlnProAlaGlnProArgLeuLeuArgArgPro 275
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-----GlyGluTyrLeuAlaAspHisArgHisArg---ProLeuSerArgAlaCysGly 393
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ProArgGlnProAlaProGlyGlyThrGlnArgProProHisPro 428
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Matches:
Conservative:
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Best Local S Query Match: DB:	ocal Similarity: 29.0% Mismatches: 166 Match: 2 Gaps: 35	Oy 1078 TACGTCCTGACCAA
US-10-	US-10-665-990A-13 (1-1561) x US-09-252-991A-24941 (1-475)	296 ArgArgProGluProArgLeuSerPheProGlyGlnProLeuArgAlaValArgAlaArg
& 8	145 CAAACCTGTCCT	Qy 1102 GGCGACCGACGTTGCCGCCGTCATTCCGGCTACGTCAATACCG 1146
<u>ک</u> ۾		Oy 1147 AAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCAACCATGCCGTCCC 1206
දු දු		Oy 1207 CGCCACAAAAGACAAAGGCCTGACCGGCAGCTCCGTAACCTGCCAGCCTGCCAAACCTT 1266
\ \ \ \ \	280 CAGCCTCGATTTGCAATACTACATTTGGCGCAACGACATTTCCGGCAGGCTGCTGTTCAA 339 :::	Oy 1267 CATTGTGGACGCCAACCTCTCATCGGCTCATTCAACCTCGACCCCGTTCGCACG 1326
රු සි		Oy 1327 GCTCAATACCGAAATGGGCGT
δ d		Qy 1363 CAAAATCGCAGAACAGATGGAGCGCACCTCGCCGATACCACCCGAATACGCCTACCG 1422
8 6	CCTGTTCAACCCCTTCGTCCTACGCAAATGGCGCGCACTCGGCTACCTGACCGACTTCCC	Qy 1423 CGTTACCCTCGACAAACACCGCCTGCAATGGCACGATCCCGCCACCCGAAAAAC 1479
ò	CCGCCTCAACCGCCGCATGCACAAATCCTTTACCGCCGACAACCG	Qy         1480 CTACCCGAACGAACCCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATCCTT 1539           DD         427 LeuProGluArgLeuArgPro 433
8 8 8	146 AlaValProProValG1yProAlaArgArgLeuGInArgArgPheProCysAlaValAla 165 568CGCCACCACCATACTCGGGGGACGCAATATCGGCGACGAATA 606 15	Qy 1540 GCTGCCCATCGA 1551  Db 434 AlaLeuHisArg 437
<u>ک</u> 8		RESULT 30 US-09-252-991A-24311 ; Sequence 24311, Application US/09252991A : Defeat No. 6561705
රු සි	CGTCGTCGGCGAAGTATCGCACGACTTCGACCGCTACTGGGCAAGCGCTTCCGCCCACAA	GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: MARC J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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6 G	784 CGACGAAACATCCAGACACGCGTCCTGCGCTACCGCGAAACGGTCGAACAGTCGCCCT 843	ATE: 1998-02 ION NUMBER: ATE: 1998-07 ID NOS: 3314
& 48	844 CTACCAAAAAATACAGACGGACGCATCGACAGAGCGTCCAAACCCGCCTGATCAG 903	SEQ ID NO 2 LENGTH: 5 TYPE: PRT ORGANISM:
ò q	904 CGACACCCCTGCAAAAGGACTCGACCGCGGCAAACCGCCGATTGCCGGGAGGCT 963	-252-991A-24311 ment Scores: No.: 4.48e-13 Length:
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oy G	1018 CGTCCCTACAAAATCCGGCACAGAGGCACTGGCAAAACTGGTGCAGGACGGCATAGACGT 1077     ::	

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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
FILE REFERENCE:
107196.136
CURRENT APPLICATION NUMBER:
US 60/074,788
PRIOR FILING DATE:
1998-02-18
PRIOR FILING DATE:
1998-02-27
NUMBER:
US 60/094,190
PRIOR FILING DATE:
1998-07-27
NUMBER:
SEQ ID NOS:
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Matches:
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Query Match:
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US-09-252-991A-30799
; Sequence 30799, Application US/09252991A
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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| ProGlyLeuPheArgArgIleAlaLysArgGlnProAlaThrArgGlyProProArgArg
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Mismatches:
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Matches:
APPLICATION NUMBER: US/09/252,991A
                  CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27502
                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27502
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363

74

522

us-10-665-990a-13.rai

ORGANISM: Pseudomonas aeruginosa -09-252-991A-17231 ignment Scores: -1.1e-12			286 ProArgArgProdlyAspAlaArgProdlyAspAlaArgProAlaProGlyAlaGly 300 496
	Qy         1087 GACCAACTCGCTACAGGACGACGTCGACTCCGGCTACTCCGGCTCCAATACCG         1146           Db         327 ArgProLeuGlnAlaHisGlnAProArgProTyrAsnTrpArgHisAlaPro         345           Qy         1147 AAAACCGCTGCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCATCGCGTCCC         1206           Db         346 GlnGlyGlyGlnGln	QY         1327 GCTCAATACCGAAATGGCGTCATCGAAAGCCCCAAAATGGCAGAACAGATGGA 1383           Db         369Arg1leArgHisProArgArgGluArgArgFroGlySerArgArgArgArgArgArgArgArgArgArgArgArgArg	RESULT 34 US-09-252-991A-17231 US-09-252-991A-17231 Sequence 17231, Application US/09252991A Facent No. 6521795 GENERAL INFORMATION: FAPPLICATION: FAPPLICATION: FAPPLICATION: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE NOWERRION: FILENCE PREDATE: FILENCE FILENCE DATE: FILENCE FILENCE DATE: FILENCE FILENCE DATE: FRIOR PRIOR FILENCE DATE: FRIOR FILENCE DATE

6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	295 LeullevalMetArghlaproSerProTyThrleuProArgProSerNlabrobeval 314 378 GCCTGCTGTGGAGGACAACAACGGGGGGGTGGACGTCTCTGGCCTGACA 477 315 GlyLeuAlaGlyLySThrProThrSerSerArgProArgAcgaCGTCTGCCGCTCTGCCTCTCCTCGCCTGACA 473 438 GCCTGCCAATATGGAAGTGCGCT	1281 AACGCATCTTCATCGG
8 8 8 8 8 8	549 'HisHisArgProValProArgAspGinAlakTgHisFloLeuProArgProArgProG1 569 1135GTCAAATACCGAAAACCGCTCCA 1160 569 yHisGlyThrProThrGlyGluAspProAlaProG1nArgLeuProArgSerAlaArgA1 589 1161 AAGCCGCCATCAAACTCTACGAGCTGCAACCAACCATCCCGCCACAAAGAA 1220 1161 AAGCCGGCATCAAACTCTACGAGCTGCAACCATGCCGTCCCCGCCACAAAGAA 1220 1161 AAGCCGGCATCAAAAGATGAACCAACCAACCATGCCGTCCCCGCCACAAAGAA 609 1221 AAGGCCTGACCGCACCCCGTAACCAGCCTGCATGCCAAAACCTTCATGTGGACGGCA 1280 1221 AAGGCCTGACCGCAACCAGCCTGCATGCCAAAACCTTCATTGTGGACGGCA 1280 16	Oy 112 AGAACGGACGGAAGCCGTCATTCAATACTTCCAAACCTGTCCTCGGACAACAT 168  (1) AGAACGGACGGAAGCCGTCATTTCAATACTTCCAAACCTGTCCTCCTGGACAACAT 168  (2) I A KGThrAspGlyArgaspArgValArgHisArgArgLeuArgAlaProProGlyGluGln 192  (3) I 69 CCTGCAAATCCGGCACCCCTCATAACAACGGCTATCCGACATCTACCTGCTCGTCGACGA 228  (4)

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Indels:
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ORGANISM: Pseudomonas
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Best Local Similarity:
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US-09-252-991A-30396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 30396
LENGTH: 694
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267 LeuAlaProLeuArgGlnArgHisProAlaGlyIleArgProGlyAlaArgHisArgGln 286
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TITGCAAIACTACATITGGCGCAACGACATITCCGGCAGGCTGCTGTTCAACCTCATGIA 348
                                                      CCTTGCCGCAGAACGCGCGCGTGCG---CGTACGCCTGCTTGGACGACAACAACACGCG 405
                                                                                                                                  247 GlyLeuGlyArgAsnProArgArgProProAlaAspGlyArgHisGlyArgProAlaAsp 266
                                                                                                                                                                  ----CGCACTCGGCTACCTGACCGACTT 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          823 AACCGTCGAACAGTCGCCCCT---CTACCAAAAATACAGACGGACGCATCGACTGGCA 879
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                                                                                                                                                                                                                                                                                                                                                                                       CGAAGTATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAAGGCCAC---
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                                                                                                                                                                                                                                                                                                                                   -----CGGCAGCGTCGTCGG
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501 AlaGlyLeuArgGlnHisGlnArgProArgAlaGlyArgLeuArgArgArgProArgArg
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                                                                                                           CGGGTTGGACGATCTCCTGCTCGCCCTCGACAGCCATCCCAATAT----CGAAGTGCGCCT
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               631 TTTCGCCGACCTGGACATCCTCGCCAC-----
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RESULT 37
US-09-252-991A-30396
; Sequence 30396, Application US/09252991A
; Sequence 30396, Application US/09252991A
; Sequence 30396, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
; TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
                                                                                                                                                                                                                                                                     1405 ACCCGAATACGCCTA------CCGCGTTACCCTCGACAAACACACCGCCT 1449
                                                    1294 CGGCTCATTCAACCTCGACCCCCGTTCCGCACGGCTCAATACCGAAATGGGCGTCGTCAT 1353
                                                                                                                                                              ---TACCAC 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      348 ACCTTGCCGCAGAACGCGGCGTGCGCGTACGCCT---GCTGTTGGACGACAACACGC 404
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------GlyHisGlyHisArgArgGlyGlnLeuArgHis---ArgAlaArgAr
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                                                                                                                                                              1354 CGAAAGCCCCAAAATCGCAGAACAGATGGAGCGCACCCTCGCCGA-
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| AlaProGly---GluArgProProGluArgLeuThrGluArg 627
GlyProArgThrAspAlaThrAlaProGlyAlaGlyGlydlyArg
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Matches:
Conservative:
Mismatches:
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us-10-665-990a-13.rai

QQ	77 oProGlyValArgHisGlyArgAlaGlnArgProAlaAlaAlaGlyAlaGlnGlyHisGl 97	
ζ	405 GCGGGTTGGACGATCTCCTGCTCGCCCTCGACAG	Qy 1231CGGCAGCTCCGTAACCTGCATGCCAAAACCTTCATTGTGGACGGCAAAC 1283  Dh
q	97 yArgLeuProGluSerProArgArgProArgGlnLeuValValHisValLeuLeuGlnAr 117	1084 COMPENDATIONS AND CONTRACT ON THE SECTION OF T
<i>ò</i>	CCATCCCAATATCGAAGTGCGCCTGTTCAACC	447 aHisAlaThrArgAlaAspProArgProGlyThrGlyProAlaSerGlyGlyArgLe
g	117 gHisLeuArgArgLeuProArgProGlyGlnHisProAlaArgLeuPheProArgPr 136	
δ a	471 CCTTCGTCCTACGCAAATGGCGCGCACTCGGCTACCTGACCGACTTCCCCCGCCTCAACC 530	
ò	GCCGCATGCACAAATCCTTTACCGCCGACAACCGCGCCACCATACTCGGCGGAC	Qy 1339 -AATGGGCGTCGTCATCGAAAGCCCCAAAATCGCAGAACAGATGGAGCGCACCC 1391
qq		486 yAspAlaClyArgClnArgHisProClnHisProAlaGlnArgArgClyAlaAlaGl
δ		OY 1392 TCGCCGATACCACACCCGAATACGCTACCGCGTTACCCTCGAAAACAAACCACCCC 1448
qq	173 oGlnProAlaAspGlyValHisProGlyArgHisLeuHisArgArgGlyArgPheProLe 193	TGCAATGGCACGATCCCGCCACCGGAAAAACCTACCCGAACGAACC
රු අ	631 -TITICGCCGACCTICGACATCCTCGCCACGGCAGCGTCGTCGGCGAAGTATCGCACGACT 689 193 uValGlakrgAspGlyArgProArgProValArqGlyArqHisAlaGlnSerArdCy 212	 
ò		1495CGAAGCCAAACTTTGGAAAGGCAT
QQ	212 sArgGlnTrpArgGlyValProValGlyThrAlaAlaLeuProGlnGlyAsnArgArgAs 232	546 YFIOLEUALAINIFALAALAINIFALAGIUALAAFGFIOA
è 5	715CGCCCACAACGCCACGCGCATCATCCGCAGCGCAACATCGGCAAGGGTCTTCAAG 770	Db 566 oAlaValAlaArgArgIleProProValProAla 577
3 3	propried and an area of the contract of the co	RESULT 38
중 음	7.1 CALLOGATACAACAACAACAACAACAACAACAACAACAACAACAAC	US-09-25z-991A-30397 ; Sequence 30397, Application US/09252991A ; Patent No. 6551795
ò	816 ACCGCGAAACCGTCGACCCTCTACCAAAAATACAGGGACGCA 869	; GENERAL INFORMATION: ; APPLICANT: Marc J. Rubenfield et al. ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
gg	lArgGlnSerArgArgAlaGlyLeuValArgProProArgGlyGluAlaAlaLeuAlaHi	; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ; FILE REFERENCE: 107196.136
දු දි	870 TCGACTGGCAGAGCGTCCAAACCGCCTGATCAGCGACACCCCTGCAAAAGGACTCGACC 929 870 TCGACTGGCAGAGCGTCCAAACCGCTGATCAGCGACACCCCTGCAAAAGGACTCGACC 929 288 811 81 81 81 81 81 81 81 81 81 81 81	HAG
} }		; PRIOR AFFELLATION NUMBER: US 00/0/4,/00 ; PRIOR FILING DATE: 1998-02-18
3 음	302 uArgGlyAlaAlaThrGluHisTrpArgGlyGlnArgLeuArgAlaSerHisGlybysPr 322	PRIOR AFFLICATION NUMBER: US 60/034,13 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
ò	TTCACCC	g ii t
Dp	322 oGlyCysAlaAlaGlyGlyHisProGlyAlaGly***GlyArgGlnGlnGl 339	; TYPE: PRT ; OKCANISM: Pseudomonas aeruginosa ; OCSANISM: Pseudomonas aeruginosa
à i	AAAACTGGTGCAGGCATAGACGTTACCGTCCT	ignment Scores:
8 8	339 yThrProAlaGlyHisArgArgCysGlnProValArgArgTrpArgFroGlyGl 358 1086	Pred. No.:         1.59e-12         Length:         894           Score:
: 음	yAlaGlnGlnProAlaSerAlaGlyProGlyLeuLeuCysAspSerGlyAsnLeuGlyHi	ity: 25.3% Mismatches: 1.1ty: 25.4% Indels:
ò		2 Gaps:
qq	:::                378 sArgAlaValProGlyProProAlaAlaGlyPlaGluProLeuAlaThrGlyGlnArg 397	-10-665-990A-13 (1-1561) x US-09-252-991A-30397 (1-894)
<u>ک</u> ج	1113 TTGCCGCCGTCCATTCCGGCTACGTCAATACCGAAAACCGCTGCTCAAAGCCGGCATCA 1172	Db 220 GlyGlnArgProGlnAlaThrArgHisGlyArgAspArgArgArgArgArgArgArgArgArgArgArgArgArgA
ì è		Qy 205CCCCCA 234
6 G	gProGlyAlaAlaArgHisProLeuHisProGlyProArgArgLeuProGlyDe	Db 240 AlaGlyThrProThrGlyProHisArgArgGlnThrProAlaArgArgAlaGlySerPro 259

264 Db 583 324 Db 603 283 Qy 1039 384 Db 623 296 Qy 1120 426 Db 643	496	597  410  410  QY  13.9 TACCACACCGA  621  Db  7.55 HisHisArgArgGly  430  QY  1443  775 ArgGlyArgGlyVal  450  QY  1444 CGGCTGCA  720  Db  795 ArgLeuProProAla  470  QY  1462 CGCCTGCA  QY  1462 CGCCTGCA  QY  1462	744 Db 490 Qy 801 Db 510 Qy 861 Db 525 RESULT 39 909 US-09-252 909 US-09-252 1 Patent 969 PRINER 545 Patent 1023 TITLE 564 TITLE 564 TITLE 564 PRIOR 1038 PRIOR
235 CGAAGCCCTTGCCGCCCCGCCCCTTAT  [			721 CAACGCCACGCCGATCATCCG
8 6 8 6 8 6	8 6 6 6 6 6 6	8 6 8 6 8 6	6 8 6 8 6 8 6 8 6 8 6 8 6

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infield et al.
LibrC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
UGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
AND THERAPEUTICS
BER: US/09/252,991A
99-02-18
3: US/09/252,991A
8: US/09/4,788
8-02-18
R: US/094,190
                                                                                                                                                                                                                               CATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCAT 1170
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                                                                                                                                      -----GACCGACGTTGCCGC 1119
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|abeuProArgGlySerLeuLeuSerGlyAlaHisGlyAlaLeuPro 814
sLeuProSerGlyProGluLeuLeuProAspLeuAspLeuAlaGly 602
                                                                                     gserAlaValAlaProAspGlnArgThrArgProArgGlnHisPro 622
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uLeuGlyGlyThrAlaAspValGlyTrpArgAspGlnArgArgArg 642
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isArgSerGlyThrArgProValGlnHisValValAlaAlaGlnGly 734
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|sGlyAlaHisProGlnGlyGlyGlyArgGlyArgGlyLysProGln 834
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	724 164 38 38 215 35	(1-724)	CCGGCACACCCCTCATAACAACGGGCTATCCGACACTTACTGCTGGACGACGACGA 237	-ArgleuleuProLeuArgAlaLeuleuGln 15	AGCCCTTGCCGCCCCCCTTATCGAATCTGCCGAACACACAGCCTCGATTTGCAATA 297	TTCAACCTCATGTACCT 351	ThrGlyArgGlyArgArgAlaGlyLysArgValLeuArgGlnProHisArgGlyLeuPro 55	CGTGCGCGTACGCCTGCTGTTGGA 390	HisArgArgValHisArgGlnAspProLeuArgAlaLeuGlnProGlnValGlyHisAla 75	CGACAACAACAC	ν 4	LeuArgArgAspFroProHisArgGluProLeuGlnArgLeuGlyGlnProLeuEuPro 115	creacceactrecececers 528	  LeuArgProArgSerLeuArgLeuArgGlnProArgArgProSerAlaProAla 135	549	:::     AlaAlaGlyAlaGluGlnAlaGluAlaGluProGlyArgArgProArgProClyArgArg 155	CTTTACCGCCGACAACCGCGCCACCAT 576	ProAlaGluGlyAlaGlnGlyGlyArgHisArgPheAlaAlaAlaArgGlnProGlyLysGln 175	ACTCGGCGGACGCAATATCGGCGACGAATACTTCAAAGTCGGTGAGGACACCGT 630		  AlaArgProProAlaProAspProAlaGlyHisAlaGlyArgProAlaAlaGlyAlaGlu 215	CATCCTCGCCACCGGCAGCGTCGTCGCGAAGTATCGCACGACTTCGACCGCTACTGGGC 705	GlyLeuArgProArgArgGly 231	CAGCGG 747		-CAAGGGTCTTCAAGCACTCGGATACAACGACGA 789	: lavalAlaArgArgArg 267
PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 LENGTH: 724 TYPE: PRT ORGANISM: Pseudomonas aeruginosa	Length: Matches: Conservative Mismatches: Indels:	-252-991A-31715	ACGGGCTATCCGACATC	Argheut	CCCTTATCGAATCTGCC 	TTTCCGGCAGGCTGCTG	::::: aGlyLysArgValLeuA	CGTGCGC	nAspProLeuArgAlaL	GCGCGGG		-CGACAGCCAICCCAAI    :::        SArgGluProLeuGlnA	-GCGCGCACTCGGCTAC	 gLeuArgLeuArgGlnP		aGluAlaGluProGlyA	CTTT	yGlyArgHisArgPheA	ATATCGGCGACGAATAC  :::      :::::  VTrpArgArgGlnLeuL		pProAlaGlyHisAlaG	TCGTCGGCGAAGTATCG	oArgArg	ccaceccarcarces-	a gargProHisArgProG	CAAGGGTCTT	sArgHisGluGlyProA
	1.76e-12 261.50 261.50 city: 32.3% ilarity: 26.2% 2.2%	-13 (1-1561) x US-09	CCGCCACACCCTCATAACA	ProLeuHis	AGCCCTTGCCGCCCGCGCCG       SlyLeuArgArgHisAr	TACATTTGGCGCAACGACA	:::     hrGlyArgGlyArgArgAl	TGCCGCAGAACGCGG	lisArgArgValHisArgGl	CGACAACAACAC      :::     alargengluHislenDr		.euArgArgAspProProHi	CTTCGTCCTACGCAAATG		CCGCCGCATGCACAACAATC-	llaalaglyalagluglnal		roAlaGluGlyAlaGlnGl	CCTCGGCGGACGCA             euArqProAlaArqAlaGl	TTTCGCCGACCTGGA	   aArgProProAlaProAs	ATCCTCGCCACCGGCAGCG	lisbroArgHisArgGlyPro	AAGCCATTCCGCCCACACGCCACGCGCATCATCCG	ProAspProAspAr	CAACATCGG	GlnGlyArgArgAspGlyCysArgHisGluGlyProAlaValAlaArg
IOR FILING THER OF SE ID NO 317 INGTH: 724 PE: PR: KGANISM: F	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarit; Query Match: DB:	-665-990A-13	178 C	w	238 A 16 G	298 C	36 T	352 T	H 95	391 -		n w	472 C	116 L	529 C	136 A	- 220 -	156 P	577 A 176 L	631 T	196 A	646 C	216 H	706 A	232 P	748 C	250 G
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976 ------CAAACAGCCCGAAAAAGCGTCTATCTGGTTTCACCCTATTT----- 1017 1042 ------GGTGCAAAACT-----GGTGCAGGA----- 1065 ----- CGTCCCTACAAATCCGGCACAGA----- 1041 1159 CAAAGCCGGCATCAAACTCTACGAGCTGCAACCCAACCATGCCGTCCCCGCCAC---- 1212 1249 ---CCTGCATGCCAAAACCTTCATTGTGGACGGCAAACGCATCTTCATCGGCTCATTCAA 1305 1306 CCTCGACCCCCCCTCCACGCTCAATACCGAAATGGGCGTCGTCATCGAAAGCCCCAA 1365 1066 ------CGGCATAGA----CGTTACCGTCCTGACCAACTCGCTACAGGCGAC 1107 1108 CGACGITGCCGCCGTCCA-----TTCCGGCTACGTCAAATACCGAAAACCGCTGCT 1158 1423 CGTTACCCTCGACAAACACAACG------CCTGCAATGGCACGATCCCGCCACCCG 1473 1366 AATCGCAGAACAGAT---GGAGCGCACCCTCGCCGATACCACCCGGAATACGCCTACCG 1422 1474 AAAAACCTACCCGAACGAACCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATCCT 1533 348 GlySerValArgGlnLeuAlaGlyGlnGlnGlyIleAspArgSerArgGlyGluHisArg 367 442 ArgArg---ArgSerProAlaAspArgHisHisArgGlnGlyAlaProGlyAlaAlaGly 460 461 GlyGlnLeuArgArgArgArgArgHisProGlyGlnProGlyArgProArgProAlaLeu 480 481 LeuProGlyValArgProAspLeuLeuArgArgGlnGluHisGlyProArgGlyLeuAla 500 382 GlyGlyArgArgSerGlnGlnProArgProGlyAlaLeuArgArgArgLeuArgGlySer 401 402 ArgAlaArgAlaThrAspLeuArgThrGlyArgArgArgGlyGlyAlaGlyGluArgSer 421 501 LeualaalaCysAspProGlnHisProAlaArgGlnAla------ArgArgLeuAsp 517 547 HisGlnGlyProGlnAlaGlyProArgThrAlaProValGlnArgAlaHisArgHisAla 566 790 AACATCCAGACACGC------GCTCCTGCGCTACCGCGAAACCGTCGAACAGTC 837 897 288 ProProArgArgArgGlyArgGlyAsnArgSerArgArgAlaGlyArgSerArgSerPro 307 898 GATCAGCGA------CACCCCTGCAAAAGGACTCGACCGCGACCG 940 CAAACCGCCGATTGCCGGGAGGCTGCAAGACGCGCT------- 975 328 AlaGlyProGlyLeuArgProAlaHisArgArgCysProAlaGlyGlyGlnAlaSerAla 347 -----GlnTyrGlnArgAlaArgAlaAla 575 838 GCCCCTCTACCAAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCT 1213 ---AAAAGACAAAGGCCTGACCGGCAGCTCCGTAACCAG-------1534 ATCCCTGCTGCCCATCGA 1551 567 Arg-----576 HisProAlaGlyHisArg 581 975 -----1018 6 B 6 8 & B 8 & 8 & g 8 6 6 원 상 원 25 da 55 da දු දු 8 g

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661 LeuHisLeuGlyThrGlyArgAlaProGlyThrGlnArgProProAla 676	TCATCGAAAGCCC		1378 GAIGGAGGCCCGAIAC 1401	 	1402 CACACCCGAATACGCCTACCG		1447 CCTGCACTGCCACGATCCCGCCACCCGAAAAACCTACCC 1485		1486 GAACGAACCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATCCT 1533	756 GlyGinAlaAsnAlaValArgGlnProLeuArgArgLysArgArgAlaGlnPro 773
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-UNITS=bits -START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-DOCALIGN=200 - TFN SCORE=pct - TFN MAX=100 - TRANS=human40.cdi - LIST=45
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-USER=US1066590 @CGN 1_1348_@runat_01052006_111938_9478 - NCPU=6 - ICPU=3
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	Description	Abp79466 N. gonorr	Abb78070 Amino aci	Aay75751 Neisseria	Aay75753 Neisseria	Aay75752 Neisseria	Adlo4719 M. catarr	Abo75163 Pseudomon	Aaw55452 H. pylori	Aaw55550 H. pylori
SUMMARIES	ΠD	ABP79466	ABB78070	AAY75751	AAY75753	AAY75752	ADL04719	AB075163	AAW55452	AAW55550
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       The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins an antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP910166 represent nucleic acid molecules of the invention
                                                                                                                                                                                                                                           ArgLysTrpArgAlaLeuGlyTyrLeuThrAspPheProArgLeuAsnArgArgMetHis
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                                                                                                                                                                                                                  Lys1leGlnAlaMetProSerGluThr1leSerProMetLysThrArgSerLeu1leSer
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                                                                                                                                                                                                        The present sequence represents a p55 polypeptide. The specification describes p177, p88, p64, p55 and p46 polypeptides from Neisseria gonorrheae. The polypeptides are useful as vaccines, for preventing, o protecting a female patient against, N. gonorrheae colonization or infection. Such immunisation can prevent gonorrhea in women. (Updated 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                        PheAlaAlaArgAlaAlaLeuIleGluSerAlaGluHisSerLeuAspLeuGlnTyrTyr
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                                                                                                                                                     New polypeptide comprising p177, p88, p64, p55 or p46 from Neisseria gonorrheae, useful for preventing, or protecting a female patient against, N. gonorrheae colonization or infection.
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Query Match:
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, Scarselli M;
                                                                                                                                  Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
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                                                                                                              Neisseria gonorrheae ORF 987 protein sequence SEQ ID NO:2974.
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Rappuoli R, Ratti G,
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                                AAY75751 standard; protein; 507 AA
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antibacterial; gene therapy
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Tettelin H, Venter JC;
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N-PSDB; AAZ54513.
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Scarselli
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Scalato E, S
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Ratti
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Pizza M, Rappuoli R,
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N-PSDB; AAZ54515.
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31-JUL-1998;
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Tettelin H,
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AAZ5301S to AAZ54536, AAZ54577 to AAZ5461S, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisserial bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols
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                                                     Claim 2; Page 1396-1397; 1453pp;
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Novel Neisserial polypeptides vaccines and diagnostics.
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY5941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54571 to AAZ5456 and AAZ54616 to AAZ5471 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Naisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols
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Scarselli
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Petersen J, Pizza M, F
Tettelin H, Venter JC;
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                                                                                                     ArgGluThrValGluGlnSerProLeuTyrGlnLysIleGlnThrGlyArglleAspTrp
                                                                                                                                                                                                         341 ValGlnAspGlylleAspValThrValLeuThrAsnSerLeuGlnAlaThrAspValAla
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                                                                                        AAGGGTCTTCAAGCACTCGGATACAACGACGAAACATCCAGACACGCGCTCCTGCGCTAC
                                                                                                                                       CGCGAAACCGTCGAACAGTCGCCCCTCTACCAAAAATACAGACGGGACGCATCGACTGG
                                                                                                                                                                                          CAGAGCGTCCAAACCCGCCTGATCAGCGACACCCCTGCAAAAGGACTCGACCGCGACCGC
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                                                                                                                                                                                                                                                                                             TATCTGGTTTCACCCTATTTCGTCCCTACAAAATCCGGCACAGACGCACTGGCAAAACTG
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The invention relates to an isolated nucleic acid encoding an Moraxella catarrhalis polypeptide. The nucleic acid is useful for preparing a composition for diagnosing, preventing or treating infection caused by Moraxella catarrhalis. The present sequence represents the amino acid sequence of a M. catarrhalis protein.
TCATTCAACCTCGACCCCCGTTCCGCACGGCTCAATACCGAAATGGGCGTCGTCATCGAA
                                                                        TACCGCGTTACCCTCGACAACACAACCGCCTGCAATGGCACGATCCCCGCCACGAAAA
                                                                                               ACCTACCCGAACCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATCCTATCC
                                                                                                      New nucleic acid encoding a Moraxella catarrhalis polypeptide, preparing a composition for diagnosing, preventing or treating caused by Moraxella catarrhalis.
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Matches:
Conservative:
Mismatches:
Indels:
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35.9%
29.2%
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                                                                                                                                                                                                                                               Moraxella catarrhalis;
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N-PSDB; ADL02799.
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Best Local Similarity:
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                                     CACAGCCTCGATTTGCAATACTACATTTGGCGCAACGACATTTCCGGCAGGCTGCTGTTC
                                                                                                    AACACGCGCGCGTTGGACGATCTCCTGCTCGCCCTCGACAGCCATCCCAATATCGAAGTG
                                                                                                                                                                    CCCCGCCTCAACCGCCATGCACAACAATCCTTTACCGCCGACAACCGCGCCACCATA
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GCCGTCCATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTC
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PheGlulleLysSerSerAlaGlnSerIleGlnAspAsnGluAsnArgPheTrpArgThr
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------ThrileGluAsnGlyGlnProValIleLeuHisHisGluProHis
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|JysSerMetThrPheAspAsnLys1leSerVal1leGlyGlyArgAsn1leGlyAsnGlu
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                AAATGGCGCGCCACTCGGCTACCTGACCGACTTCCCCCGGCTCAACGGCCGCATGCAAC
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                                                                ProHisLeuProLysSerLeuAlaLeuThrLysGlnValGlnGluArgHisGlnMetVal
                                                                                                                                             CCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACGACCCCCACGAAGCCCTTGCC
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                  The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therefore the polymucleotides encoding them. The sequences are useful in diagnosis and therefore the sequences are useful in diagnosis and the parthological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions are allting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bhind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for accombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is a H. pylori secreted protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. C. a vaccine to prevent or treat H. pylori infection or to identify H. C. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific critical sequences of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify clikely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant cand determined the sequences of interest, particular regions can be included from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in B. coli hosts
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|I|eSerTyrAspProTyrThrThrThrIleGlySerLeuTyrAlaLysAsnLeuLysGlu 49
                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection.
                                                                                                   activator;
                                                                                    Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
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                                                           H. pylori ORF 02ae11612_33203250_c1_51 secreted protein.
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28-OCT-1996;
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GGCATCAAACTCTACGAGCTGCAACCCAACCATGCCGTCCCCGCCACAAAAGACAAAGGC 1225
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AspLeuSerSerGlnValIleAlaLysGluLeuLeuAsnAlaAlaAsnArgGlyValLys 109
                                                                                                                                                                                                                                                                                                    ----GATCTC 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                   244 GluileAlaLysLeuHisGluLysIleProileSerAlaGluAspAlaAsnGluPheGlu
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                          GCCGCCCTTATCGAATCTGCCGAACACACCTCGATTTGCAATACTACATTTGGCGCAAC
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CTGACCGGCAGCTCCGTAACCAGCCTGCATGCCAAAACCTTCATTGTGGACGGCAAACGC 1285
                                                                                                                GTCGTCATCGAAAGCCCCCAAAATCGCAGAACAGATGGAGCGCACCCTCGCCGATACCACA 1405
                                                                                                                                                                       GCCACCCGAAAAACCTAC------CCGAACGAACCGAAGCCAAACTTTGGAAA 1513
                     431
                                                                                                                                                                                                        467
                                                                                                                                                                                                                                                        This sequence is a H. pylori secreted protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of the pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoasaays
                                                                     412 ThrLeuleuGlySerPheAsnIleAspProArgSerAlaTyrIleAsnThrGluSerAla
                                                                                                                                 ---GlnGlnSerTrpHisLeuValLeuTyrArgHis---ArgVallleTrpGlu----
                                                      1286 ATCTTCATCGGCTCATTCAACCTCGACCCCGTTCCGCACGGCTCAATACCGAAATGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic, vaccine, prevention, treatment, infection, envelope, identification, binding compound, bacteria, life cycle, activator, inhibitor, duodenal ulcer disease, chronic gastritis, diagnosis.
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                                                                                                                                                                                                                                                                                         CGCATCGCCGCAAAATCCTATCCCTGCTGCCC 1546
                                                                                                                                                                                                                                                                                                              488 ArgLeulleLysGluTrpSerLysValLeuPro 498
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25-OCT-1996;
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to evaluate the abundance and distribution of H. pylori-specific antigens. The genemic sequence of H. pylori (ATCC 55679) was determined brown overlapping contigs generated by mechanically shearing the bacterial brown. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts
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50 AsnProLysHisSerAlaAlaIleLeuLeuGluAspGlyPheAspAlaLeuLeuHisArg
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51.7%
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Best Local Similarity:
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N-PSDB; AAX14097.
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Best Local Similarity:
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24-JUN-1997;
                   29-JUL-1997;
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--AsnAlaIlePheLeuAlaAspLeuProAlaLys---Ile
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355 ThrAspAlaIleValValTyrGlyAlaTrpGluArgTyrArgAsnLysLeuValArgMet
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---GlnGlnSerTrpHisbeuValLeuTyrArgHis---ArgVall1eTrpGlu-----
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                                                                                                                                                                                                                                                       This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis
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                                                                                                                                                  New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases.
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| AsnGlnLeuValArgMetGlyAlaAsnValTyrGluIleArgAsnAspPhePheAsnArg
                                                                                                                                                                                                                                                                                                                                 GCCACAAAAGACAAAGGCCTGACCGGCAGCTCCGTAACCAGCCTGCATGCCAAAACCTTC
                                                                                                                                                                                                                                                                                                                                                                                     ACATCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGTCGCCCCTCTACCAA
                                                            LysileProlleSerAlaGluAspLysAsnGlnPheGluLysLysValAsnAspPhelle
                                                                                  ----ATCAGCGAC
                                                                                                                                                                               235 LysAlaLeuLysAsnAlaLysAspSerValPheIleAlaSerSerTyrPheIleProGly
                                                                                                                                                                                                         AAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGACGGCATAGACGTTACCGTCCTG
                                                                                                                                                                                                                                                 ACCAACTCGCTACAGGCGACGTTGCCGCCGTCCATTCCGGCTACGTCAAATACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -------ArgleuSerleulysAsphisAlaGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---HisArgVallle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obacter baumannii, bacterial disease; antibacterial; vaccine; biocontrol agent.
                                        AAAATACAGACGGGACGCATCGACTGGCAGAGCGTCCAAACCCGGCCTG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGAAACGCATCGCCGCAAAAATCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnSerTrpHisLeuValValTyrArg
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New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
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IleIleArgAlaAlaAspArgGlyValLysValArgLeuLeuIleAspAspAsnAsnAla
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Matches:
Conservative:
Mismatches:
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(GENO-) GENOME THERAPEUTICS CORP.
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223

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US-10-665-990A-13 (1-1561) x ADA34304 (1-275)
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                                                                            703
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211 GlyargasnMetThrasnGlnTyrTyrasnValSeraspSerTyrGlnPheSeraspVal
                                                                                           CTCAACCGCCGCATGCACAACAATCCTTTACCGCCGACAACCGCGCCACCATACTCGGC
          GGACGCAATATCGGCGACGAATACTTCAAAGTCGGTGAGGACACCGTTTTCGCCGACCTG
                                                                            GACATCCTCGCCACCGGCAGCGTCGTCGCGAAGTATCGCACGACTTCGACCGCTACTGG
                                                                                                                                                                                                                                                             Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
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100
51
78
15
                                                                                                                                251 AsnHisGluTyrAlaTyrSerValGlnSerIleValArg 263
                                                                                                                  GCAAGCCATTCCGCCCACACGCCCACGCGCATCATCCGC
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                            THERAPEUTICS CORP
                                                                                                                                                                              ADA34304 standard; protein; 275
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478.50
61.9%
41.0%
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                                                                                                                                                                                                                                                                                          Acinetobacter baumannii
                                                                                                                                                                                                                                                                      biocontrol agent
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N-PSDB; ADA30178.
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                                                                                                                                                                                                GAAAAAAGCGTCTATTTCACCCTATTTCGTCCCTACAAATCCGGCACAGACGCA 1045
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|GluProGluMetLysTrpTrpGlnLysAlaGlyMetLysLeuLeuSerTrpLeuProLeu 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGCAAAACTGGTGCAGGACGGCATAGACGTTACCGTCCTGACCAACTCGCTACAGGCG
                            GGCATCAAACTCTACGAGCTGCAACCC-----AACCAT
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                                                                                                   GACCGCGACCGCCGCAAACCGCCGATTGCCGGGAGGCTGCAAGACGCGCTCAAACAGACCC
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551 700 571 760 588 820 909

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TATITICGICCCIACAAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAG-----GAC 1066
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       IleLeuGlyAlaLeuSerGlyAlaHisGlnAsnPheGlnLeuArgValTyrAsnProThr 491
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|PheGlyLysAlaArgLeuAsnTyrPheAspTyrAlaGlySerValLeuCysCysPheArg
                                              -CIGACCGACITCCCC
                                                                                                                    CGCCTCAACCGCCGCATGCACAAATCCTTTACCGCCGACAACCGCGCCACCATACTC
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                                                                                                                                                                                                                                                                                                    ArgAspValLeuIleAlaGlyProGluAlaArgAlaMetAlaAlaAsnPheAspAlaPhe
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| GluArgValGlnArg-----ValSerAlaGluAlaAsnAspMetAspPheVal
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SerGluValGluThrArgLeuLeuArgThrGluThrArgProSerPheLeuGlySerLys
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                                                                                                                                           TrpHisAlaArgArgSerValProAlaGluArgLeu------AsnAspValGlyArg
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782 AlaValAsnLysProLeuProValThrArgLysGlyAlaArgMetGly------
                                            TTCGTCCTACGCAATGGCGCGCACTCGGCTAC---
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                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the stressness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                   cold
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                                                                                                                                                                                                                                                            New stress-responsive nucleic acid, useful for altering the responsiveness of a plant, e.g. cereal, to an abiotic stress such stress, salt stress or osmotic stress.
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Matches:
Conservative:
Mismatches:
Indels:
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T, Provart N, Ricke D, Zhu T;
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                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 6464; 89pp; English.
                                                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                    22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314652P.
26-SEP-2001; 2001US-033277P.
21-NOV-2001; 2001US-0332132P.
21-JUN-2002; 2002WO-US019668
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DB:
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Moughamer
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                                                                                                                                                                                                                                                                TCCTTTACCGCCGACAACCGCCGCCACCATACTCGGCGGACGCAATATCGGCGACGAATAC 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 TyrclucinLeuHisHisGluAspHisSerLeuThrGluAspLysLeuTyrAspAlacin
                                             GCCCGCCCCCTTATCGAATCTGCCCAACACACCCTCGATTTGCAATACTACATTTGG
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| PheGluAlaSerSerLysPheGlnPheThrAspMetAspIleLeuPheTyrGlyHisAla
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                           CCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACGACCCCCACGAAGCCCTTGCC
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1367 ATCGCAGAACAGATGCAGCGCCACCCTCGCCGATACCACCCGAATACGCCTACCGCGTT 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTCTCTGTTCATGTTCATGGTTG-----CCCCCACTGGAAGAAGAACGACGGAAGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ++ 11eVallleLysThrAsnAsnArnTrpLeuAsnAspGluAlaAlaGluGluLysThrGln--- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                           -----ÀlàGluSerIle
                                                                      LeuArgAspIleHisProGlnAsnSerTrp-ThrValAlaProArgAlaLysPro 863
                                                                                                                                                                                                                                                 Acinetobacter baumannii; bacterial disease; antibacterial; vaccine; plant biocontrol agent.
                                                      ACCCTCGACAAACACAACGCCTGCAATGGCACGATCCCGCCACCCGAAAAACCT
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Matches:
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                                                                                                                                                                                                                     Acinetobacter baumannii protein #3559
                                                                                                                                     ADA36398 standard; protein; 321 AA
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                         837 PheAlaGluGlnLeu----
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409.00
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Best Local Similarity:
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N-PSDB; ADA32272.
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Molino

Maimonis P, Lewis M;

Thiagalingam A, A, Thibodeau S,

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Detecting expression of one or more nucleic acid sequences in biological sample, useful for detecting cancer, comprises detecting a change in the expression level of one or more nucleic acid sequences relative to a
                             BAYER HEALTHCARE LLC.
MAYO FOUND MEDICAL EDUCATION & RES.
                                                                                                                         Claim 20; SEQ ID NO 178; 256pp; English.
      01-NOV-2004; 2004WO-US036404.
                  04-NOV-2003; 2003US-00700439
                                               Myerow S, The
Boardman LA,
                                                                                                             control expression level.
                                                                  2005-372198/38
                                                                       N-PSDB; AEA04440.
REFSEQ; NP_002448.
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The invention relates to detecting differential expression of one or more nucleic acid sequences (appearing as ARA0456-ARA0448) in a biological sample comprising obtaining the sample from a subject, and detecting a change in the expression level of one or more nucleic acid sequences, relative to a control expression level of the nucleic acid sequences, is new. Also included are detecting cancer (or a pre-malignant condition thereof) in a subject (comprising comparing the expression level of one or more nucleic acid sequences in each of concern control expression level of the nucleic acid sequences, where a change of at least two-fold in the expression level of the nucleic acid sequences is indicative of cancer or pre-malignant condition) in a subject (by detecting in a pological sample from the nucleic acid sequences, repetating the first step at a subsequent point in time condition in a subject (by detecting in a ploiggical sample of the expression level is indicative of progression level detected, where a change in the expression level is indicative of progression level is indicative of progression level detected, where a change in the expression level is indicative of progression level detected, where a change in the expression level is indicative of progression level of progression level of the subject), determining the expression level is indicative of progression level with a reference progression level of the subject of the subject (comparison), determining the efficacy of a test compound for inhibiting cancer in a subject, inhibiting cancer in a subject, inhibiting cancer in a subject, inhibiting cancer in a subject, inhibiting cancer in a subject, inhibiting cancer in a subject, inhibiting cancer in a subject, inhibiting cancer in a subject, inhibiting cancer in a subject, inhibiting cancer in a subject, inhibiting cancer in a subject. Inhibiting cancer in a subject or and prognosis for an experience and electring in a prognosis for an experience and electring in a prognosis for an experience and elect

8.08e-16 336.50 33.6% 24.1% Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match: DB: Best Local

Sequence 5178 AA;

US-10-665-990A-13 (1-1561) x AEA04533 (1-5178)

5178 141 55 198 190 22

Matches: Conservative: Mismatches:

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CTCGACCGCGACCGCCGCAAACCGCCGATTGCCGGGAGGCTGCAAGACGCGCTCAAACAG
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                                   CCCGAAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCCTACAAAATCCGGCACAGAC
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10-JAN-2000; 2000US-0048031.
15-FEB-2000; 2000US-00519449.
66-MAR-2000; 2000US-005194449.
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The present invention describes colon tumour associated proteins (I) and the present invention describes colon tumour associated proteins (I) and (II) can be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to trreat disorders associated with decreased expression by rectifying contextions or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and activity. The anti-(I) artibodies may also be used as diagnostic agents for detecting the presence of TCAPs in an assays to identify modulators of antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in the activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in the exemplification of the exemplification of the expression of a mine activity of antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in the exemplification of the exemplification of the exemplification of the exemplification of the exemples in the exemplification of the exemples in the exemplification of the exemples in the exemples in the exemples in the exemples in the exemples in the exemples in the exemples in the exemples in the exemples in the e
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                                                                                                                                                                                                                                   JA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Colon tumor associated proteins and nucleic acids useful for prevention, diagnosis and treatment of colonic cancer.
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19-MAY-2000; 2000US-00575251.
29-JUN-2000; 2000US-00609448.
28-AUG-2000; 2000US-00649811.
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r MJ, Stolk JA;
Clapper JD, Skeiky YAW;
                                                      TCCGTAACCAGCCTGCATGCCAAAACCTTCATTGTGGACGGCAAACGCATCTTCATCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide, useful for the preparation of a composition for stimulating an immune response against, or treating, cancer.
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Wang T, Jiang Y, Smith CL, King GE, Wang A, Clappe
Fanger GR, Vedvick TS, Carter D;
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03-AUG-2001; 2001US-00922217.
19-DEC-2001; 2001US-00025380.
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	development of cancer in a patient. (I) have immunostimulant and	ò	696GCTA
ខូខូខូ	cytostatic activities and can be used in vaccines. AB232646 to AB233725 and ABP55431 to AB55391 represent human colon cancer/tumour related	qa	    1494 OProProThrT
	sequences used in the exemptitication of the present invention	ò	749 AACATCGGCAA
) ) (	sequence 51/9 AA;	Ор	:::  S14 rThrThrLeu-
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}	したことをあるというとは、これをは、これをは、これをは、これをは、これをは、これをは、これに、これをは、これをは、これをは、これをは、これをは、これをは、これをは、これをは	δ	1043 GCACTGGCAAA
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ò	581 GCCGGACGATATCGCCGACGAACACTTCAAAGTCGGTGAGGACACCGTTTTCGCCGAC 640	RESULT ABO072	18 58 5007770 21073
qq		a x c	ABO07258 standard; p
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qq	1474 rThrThrProSerProProThrThrThrProSerProProThrThrThrThrThrThrPr 1494	XX	Ö

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                                                                                     AGGGTCTTCAAGCACTCGGATACAACGACGAAACATCCAGGACACGCGCTC 808
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us-10-665-990a-13.rag

Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder. ፫ Francis-Lang H, Belvin M, 05-JUN-2001; 2001US-0296076P. 10-OCT-2001; 2001US-0328605P. 15-FEB-2002; 2002US-0357253P. 03-JUN-2002; 2002WO-US017382. Friedman L, Plowman GD, (EXEL-) EXELIXIS INC WPI; 2003-156859/15. N-PSDB; ACD13431. WO200299122-A1. Homo sapiens 12-DEC-2002 

Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in Drosophila.

Funke RP;

Ď,

Example 2; Page 623-639; 678pp; English.

The invention relates to identifying (M1) a candidate p53 pathway condulating agent, by contacting an assay system comprising a purified HM modulating agent, by contacting an assay system comprising a purified HM Drosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored, modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a pstient (comprising contacting the cell with an agent that comprising contacting the sample with a probe for HM expression; (C) comparing the results with a control; and (d) determining whether the comparison indicates a likelihood disease) (M1) is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, contieration disorders (e.g. cancer). Another two new methods (M2 and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell crodification of the cell, so that the cell undergoes normal comparison or progression through the cell undergoes normal comparing the p53 pathway such as angiogenic, also useful for medulating the p53 pathway such as angiogenic, also useful for treating defects in the p53 pathway such as angiogenic, concert coll proliferation disorders. The present sequence also useful for treating defects in the p53 pathway such as angiogenic, concerts a buman p53 pathway modifying protein

Sequence 5179

5179 141 55 198 190 22 Conservative: Mismatches: Length: Matches: Indels: 8.08e-16 336.50 33.6% 24.1% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

US-10-665-990A-13 (1-1561) x ABO07258 (1-5179)

1267 1327 1387 1407 1422 1456 1293 ||| pGlyValCysGlyAlaProGluAspIleGluCysArgSerValLysAspProHisLeuSe 1347 1441 1474 ------ProbysteucyscysteuTrpSerAs 1307 1347 rLeuGluGlnHisGlyGlnLysValGlnCysAspValSerValGlyPheIleCysLysAs 1367 1494 1514 1529 286 226 380 -----ThrProlleThrProPr 1550 344 380 400 460 520 580 640 695 748 808 GACCCCCACGAAGCCCTTGCCGCCCCGCCCCTTATCGAATCTGCCGAACACAGCCTC pTrp1leAsnGluAspHisProSerSerGlySerAspAspGlyAspArgGluProPheAs nGluAspGlnPheGlyAsnGlyProPheGlyLeuCysTyrAspTyrLysIleArgValAs ATCCTGCAAATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGAC --SerSerTh GATTIGCAATACTACATTIGGCGCAACGACATTICCGGCAGGCTGCTGTTCAACCTCA--ACGCGCGGCTTGGACGATCTCCTGCTCGCCCTCGACGACCCATCCCAATATCGAAGTGCGC CTGTTCAACCCCTTCGTCCTACGCAAATGGCGCGCACTCGGCTACCTGACCGACTTCCCC CGCCTCAACCGCCGCATGCACAACAATCCTTTACCGCCGACAACCGCCCACCATACTC GGCGGACGCAATATCGCCGACGAGTACTTCAAAGTCGGTGAGGACACCGGTTTTCGCCCGAC -----ProileSerThrThrThrThrProProProThrThrThrProSerProProTh 641 CTGGACATCCTCGCCACCGGCAGCGTCGTCGCGAAGTATCGCACGACTTCGACC----1494 OProProThrThrProSerProProMetThrThrProIleThrProAlaSerTh 749 AACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAAACATCCAGACACGCGCTC CTGCGCTACCGCGAAACCGTCGAAC----AGTCGCCCTCTACCAAAAATACAGACG GGACGCATCGACTGGCAGAGCGTCCAAACCCGGCTGATCAGCGACACCCCTGCAAAAGGA -----TGTACCTTGCCGCAGACGCGGCGTGCGCGTACGCC-----rProProProThrThrThrThrLeuProProThrThrThrPro ACGGAAAGCCGTCATTTCAAT--TGCTGTTGG----rhhrprothr----rValleuSerThrThr--------167 1267 1287 1307 1327 119 227 287 344 1367 401 1407 1293 345 380 380 381 1423 1457 1474 1529 521 809 863 1545 461 581 969 g ò qq ò 셤 ò 원 ò 셤 ò g ò 셤 ò a ઠે g ઠે g d g g ò ò ò ò a ò g ò g ò 유

us-10-665-990a-13.rag

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The invention discloses a composition comprising two or more isolated rate or human polynuclectides or a polynuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynuclectide, a host cell comprising the vector, a method for identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a gent to perform the method, an array, a method for identifying an agent that is differentially expression of the polynuclectide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynuclectide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound for identifying a compound useful in treating compound for identifying a compound useful in treating compound that animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates its activity is useful for preparing a medicament for treating compulates. The sequence presented is a human protein (described in Table 3 for the specification, but was obtained in electronic form directly from WiPo at the specification, but was obtained in electronic form directly from WiPo at the compulation of th
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                                                                                                                                                                                         New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                        WPI; 2003-268312/26
                                                                                                                                                        GENBANK; NP_002448.
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(FARB ) BAYER AG.
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                          1094 TCGCTACAGGCGACGTTGCCGCCGTCCATTCCGGCTACGTCAAAT----
                                                                                                                                      1043 GCACTGGCAAAACTGGTGCAGGACGGCATAGACGTTACCGTCCTGACCA----
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derivative or allelic variation of the n claimed are a vector comprising the nove		1143	ολ
		rThrThrProProProfilrThrThrProSerProProThrThrThrThrThrThrThrProPr	ପ୍
Claim 1; Page; 1017pp; Engl	- H	1094 TCGCTACAGGCGACGGAGGCGTGCCGTTCGGGCTACGTCAAT 1142	ζ
New composition comprising two or more i preparing a medicament for treating pain	PT PT	ThrileThrTh	i 8
WPI; 2003-268312/26. GENBANK; Q02817.	# # # # # # # # # # # # # # # # # # #	ThrThrProS	අ ර
Woolf	TH XX	983 CCGAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCCTACAAAATCCGGCACAGAC 1042	δ
(GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.	PA PA		7 a
14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0345382P. 26-NOV-2001; 2001US-0333347P.	<u>ዋ ዋ ዋ ኛ</u>	::: 1545ThrProlleThrProPr 1550 923 CTCTACCACCACCARA CCACCARANCACACACACACACACACACACACACACACAC	qa X
14-AUG-2002; 2002WO-US025765.	P P XX	CCCCTGCAAAAGGA 9	ð
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WO2003016475-A2.	XX Nd	rinfinfueu	g (
Homo sapiens.	xx So	AACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAAACATCCAGACACGCGCTC	ò i
Human; pain; neuronal tissue; gene thera spinal segmental nerve injury; chronic c spared nerve injury; SNT. Ching	KW. KW.	:::	qa
Human Protein Q02817, SEQ ID NO 10430.	S S S S S S S S S S S S S S S S S S S	696GCTACTGGGCAAGCCATTCCGCCCACACGCGCGCATCATCGCGGGCGCG 748	ò
29-JAN-2004 (first entry)	XX	641 CTGGACATCCTCGCCACCGCAGCGTCGTCGGCGAAGTATCGCACGTTCGACC 695	જે દ
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RESULT 20	A RE	GACGAATACTTCAAAGTCGGTGACGACACGTTTTCGCCGAC	ìò
rThrLeuPro	ැ අ 	521 CGCCTCAACCGCCGCATGCACAACAAATCCTTTACCGCGGACAACCGCGCCACCATACTC 580 13.1	જે દ
1725 oThrThrMetThrThrProSerProThrThr	aa 8		qa
	δ : —	461 CTGTTCAACCCCTTCGTCCTACGCAAATGGCGCGCACTCGGCTACCTGACTTCCCC 520	ò
	<b>Q</b>	1407 rProProProThrThrThrThrThrThrEuProProThrThrPro1422	S G
1418 TACCGCGTTACCCTCGACAAACACAAACGGCC	ò	plysCyslleThrThrProSerProProThrThrProSe	a a
1358 AGCCCCAAAATCGCAGAACAGATGGAGCGCP :: -	δ a	381 -TGCTGTTTGG	δ
	ସ୍ପ -	1367 nGluAspGlnPheGlyAsnGlyProPheGlyLeuCysTyrAspTyrLysIlcArgValAs 1387	qa
1298 TCATTCAACCTCGACCCCGTTCCGCACGGC	ò		ò
1650 rProProThrThrThrProSerProPro	<del>ු</del>	rLeuGluGlnHisGlyGlnLysValGlnCysAspValSerValGlyPhelleCysLysAs	ga O
1238 TCCGTAACCAGCCTGCATGCCAAAACCTTCA	δ		λΌ
		345TGTACCTTGCCGCAGAACGCGCGTGCGCGTACGCC 380  1327 nGlvVa	ර සි
1613 OPIOThrThrThrProSerProProThrThi	<u> </u>	1307 pTrplleAsnGluAspHisProSerSerGlySerAspAspGlyAspArgGluProPhaAs 1327	QQ

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roProProThrThr------ThrThrTh 1650
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                                   CGCCACAAAAGACAAAGGCCTGACCGGCAGC 1237
                                                                                                                 CATTGTGGACGCAAACGCATCTTCATCGGC 1297
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constriction injury; CCI;
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comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polymucleotides a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating continuous and animal of one or more of the polymetides given in the specification, a method for identifying a compound useful in treating continuous and a pharmaceutical composition comprising the one or more of polymetides or their antibodies. The polymucleotide or the compound that condulates its activity is useful for preparing a medicament for treating continuous (CI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human procein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed continuous contin Etp.wipo.int/pub/published\_pct\_sequences 

Sequence 5179 AA;

||| |1327 pGlyValCysGlyAlaProGluAspIleGluCysArgSerValLysAspProHisLeuSe 1347 1347 rLeuGluGlnHisGlyGlnLysValGlnCysAspValSerValGlyPheIleCysLysAs 1367 1387 nCysCysTrpProMetAspLysCysIleThrThrProSerProProThrThrThrProSe 1407 .----SerSerTh 1293 1307 pTrpIleAsnGluAspHisProSerSerGlySerAspAspGlyAspArgGluProPheAs 1327 1367 nGluAspGlnPheGlyAsnGlyProPheGlyLeuCysTyrAspTyrLysIleArgValAs 1387 GACCCCCACGAAGCCCTTGCCGCCCCGCGCCCTTATCGAATCTGCCGAACACACGCCTC 286 287 GATTIGCAATACTACATTIGGCGCAACGACATTICCGGCAGGCTGCTGTTCAACCTCA-- 344 ------ACTICCAAACCIGICCICCIGGACAAC 166 ATCCTGCAAATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGAC ---ACGACAACAAC -----TGTACCTTGCCGCAGAACGCGGCGTGCGCGTACGCC------5179 141 55 198 190 Length:
Matches:
Conservative:
Mismatches:
Indels: (1-5179)Gaps: US-10-665-990A-13 (1-1561) x ADD44998 119 ACGGAAAGCCGTCATTTCAAT--8.08e-16 336.50 33.6% 24.1% 11.8% 1287 rihrProihr-----381 -TGCTGTTGG-----Percent Similarity: Best Local Similarity: Query Match: DB: 380 ----ignment Scores: 380 167 345 344 227 ò g a ò g a В ò 셤 ò a g ò a ò à ઠે õ

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401 ACGCGCGGGGTTGGACGATCTCCTGCTCGCCTCGACAGCCATCCCAATATCGAAGTGCGC 460

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1708 olle-----ThrThrThrThrThrProSerSerThrThrThrProSerProProPr
                    1478 ACCTACCCGAACGAACCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATCCTATCC 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises a method for diagnosing colon cancer in an individual, the method involves obtaining a serum sample from the individual and detecting the presence of either TIMP1 or Reg1-alpha and an additional colorectal cancer-associated marker. The method of the invention is useful for diagnosing colon cancer in an individual. The present amino acid sequence represents a human colorectal cancer-sssociated protein of the invention.
                                        1725 oThrThrMetThrThrProSerProThrThrThrProSerProProThrThrMetTh
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Maimonis PJ,
I, Molino GA;
                                                                                                                                                                                                                                                                                                                                                                                       Boardman LA, Bugart LJ, Burgess CC,
Huntress M, Johnson KA, Lewis ME, 1
er SLA, Thiagalingam A, Thibodeau SN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
                                                                                                                                                                                       Human colorectal cancer-associated protein #50.
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Indels:
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(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES
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                                                                                                                                                                                                           human; colon cancer; TIMP1; Reg1-alpha; colorectal cancer-associated marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; SEQ ID NO 121; 433pp; English
                                                                                                                          ADQ29695 standard; protein; 5179 AA
                                                                                                                                                                                                                                                                                                       15-DEC-2003; 2003EP-00257868.
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336.50
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                                                             1538 CTGCTGCCCA 1547
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N-PSDB; ADQ29628.
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Dwivedi P, Huntren
Brown-Shimer SLA,
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CCCGAAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCCTACAAAATCCGGCACAGAC 1042
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                                                                                                       TCGCTACAGGCGACCGACGTTGCCGCCGTCCATTCCGGCTACGTCAAAT------
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                                                   GCACTGGCAAAACTGGTGCAGGACGGCATAGACGTTACCGTCCTGACCA--
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N-PSDB; ADQ80262.
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The invention relates to a method of identifying a mammal that will respond therapeutically to a method of treating cancer by administering an epidermal growth factor receptor (EGRR) modulator by comparing the level of a biomarker in a mammal before and after exposure to an EGRR modulator. The method comprises: (a) measuring, in the mammal, the level of at least one biomarker identified in the specification; (b) exposing the mammal to the EGRR modulator; and (c) measuring in the mammal the level of the biomarker, where a difference in the level in step (c) compared to step (a) indicates that the mammal will respond therapeutically to the method of treating cancer. The method and biomarkers are useful for identifying a mammal that will respond therapeutically to a method of treating cancer by administering and therapeutically to one of the biomarkers whose levels of expression is measured in the method of the invention. will respond therapeutically to a method of comparing the level of a biomarker in a mammal to an epidermal growth factor receptor (EFGR) ID NO 151; 520pp; English. treating cancer comprises before and after exposure Identifying a mammal that Disclosure; SEQ modulator 

Sequence 5179 AA;

||| :::||||||||| ||| ThrvalGluLysHisPheAsnlleCysSerlleThrThrArgPro-SerThrLeuThrTh 1267 ||| pGlyValCysGlyAlaProGluAspIleGluCysArgSerValLysAspProHisLeuSe 1347 1387 nCysCysTrpProMetAspLysCysIleThrThrProSerProProThrThrThrProSe 1407 rLeuGluGlnHisGlyGlnLysValGlnCysAspValSerValGlyPheIleCysLysAs 1367 GACCCCCACGAAGCCCTTGCCGCCCCCCCCTTATCGAATCTGCCGAACACAGCCTC 286 -----SerSerTh nGluAspGlnPheGlyAsnGlyProPheGlyLeuCysTyrAspTyrLysIleArgValAs pTrp1leAsnGluAspHisProSerSerGlySerAspAspGlyAspArgGluProPheAs GATTTGCAATACTACATTTGGCGCAACGACATTTCCGGCAGGCTGCTGTTCAACCTCA-------TGTACCTTGCCGCAGAACGCGGCGTGCGCGTACGCC-----ATCCTGCAAATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGAC 5179 141 55 198 190 Matches: Conservative: Mismatches: ACGGAAAGCCGTCATTTCAAT------Length: Indels: (1-5179)US-10-665-990A-13 (1-1561) x ADQ80379 8.08e-16 336.50 33.6% 24.1% 1287 rThrProThr------11.8% -----Percent Similarity: Best Local Similarity: Alignment Scores: 119 1248 1293 1327 1347 1367 287 344 1307 345 167 227 380 380 381 Query Match: DB: No.: ò 셤 ò g ò a õ g 8 g ò 원 ò g ŝ a ò 원

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1725 oThrThrMetThrThrProSerProThrThrThrProSerProProThrThrThrMetTh 1745
  1708 olle-----ThrThrThrThrThrProSerSerThrThrThrProSerProProPr
                            1478 ACCTACCCGAACGAACCCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATCCTATCC 1537
                                                                                                                                                                                                                                                         Colon tumor; breast tumor; pseudomyxoma peritonei; prostate cancer; andrology; genitourinary disease; neoplasm; endocrine disease; gynecology and obstetrics; gastrointestinal disease; cytostatic; mucin; RNA interference; RNAi; gene silencing; gene therapy.
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23-JAN-2004; 2004US-0538740P.
04-JUN-2004; 2004US-0577002P.
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                                     CTGTTCAACCCCTTCGTCCTACGCAAATGGCGCGCCACTCGGCTACCTGACCGACTTCCCC
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The present invention provides polynucleotides that inhibit expression of polypeptides such as the ubiquitin conjugating enzyme UbcH7, the ubiquitin protein ligase E6-AP, mucin-1 or mucin-2. The polynucleotides considers may be RNA polynucleotides that include a sense strand and an antisense strand. The sense strand of the RNA polynucleotide comprises a sequence of 16-30 nucleotides that is substantially identical to consecutive nucleotides and mRNA encoding the target polypeptide. The consecutive administration can be to a subject, preferably a human, and can occur during surgical resection of a tumor or resection of mucinous material. Claimed methods for treating cancer include administering a polynucleotide, preferably an RNA polynucleotide, of the invention to a subject that has, or is a trisk for, an endocrine-related cancer, such as the consection of an encoring coverproduction, such as colon cancer, breast cancer or pseudomyxoma coverproduction, such as colon cancer, breast cancer or pseudomyxoma coverproduction, such as sociated with the cancer is decreased. The present sequence is that of human intestinal mucin. mRNA for MUC2 represents a target for gene silenoing using RNA polynucleotides of the invention AEA27627 and AEA27630. New RNA polynucleotide, encoding a UbcH7, E6-AP, mucin-1, or mucin-2 polypeptide, useful for treating cancer, e.g. breast, prostate, or colon

1.00	Qy         809 CTGCGCTACCGCGAAACCGTCGAACAGTCGCCCTCTACCAAAAATACAGACG 862           Db         ::              1529 rThrThrThrProProProThrThrThrProSerProProThrThr.           Cy         863 GGACGCTCGAGAGCGTCCCAAACCGCCTGATCAGCGACACCCTGCAAAAGGA 922           Db         1545ThrProIleThrProPr 1550           Cy         923 CTCGACCGCGGACGCCCGCAAACCGCCGGAGGCTGCAAACAG 982           Cy         923 CTCGACCGCGACCGCCGAAACCGCCGGAGGCTGCAAACAG 982	1550 othrestripthriptoners. Leuproners of the properties of the pr	1583   F	QY         1178 TACGAGCTGCAACCATGCCGTCCCGGCCAAAAAGACAAAGGCCTGACCGGCAGC 1237           16	1650 rproproprothrThrThrProSerProProThrThrThrProSerProProIl 1298 TCATTCAACCTCGACCCCCGTTCCGCACGGCTCAATACCGAAATGGGCGTCGTCAACGAA 1::	1358 AGCCCCAAAATCGCAGAACAGATGGAGCGCCCCTCGCCGATACCACACCCGAATAGCCC :::    :::     :::::   1689 OSETPTOPTOTHTThrThtMetThrThrProSerSerProThrThrThrThrProSerSerProThrThrThrProSerSerProThrThrThrThrProSerSerProThrThrThrThrThrThrThrThrThrThrThrThrThrT	OY 1478 ACCTACCGAACCGAACCCGAACTTTGGAACGCATCGCGCAAAATCCTATCC 1537  Db 1725 OThrThrProSerProThrThrProSerProFroThrThrThrThrThrMetTh 1745  OY 1538 CTGCTGCCA 1547  Db 1745 rThrLeuPro 1748	RESULT 24 ABUS3160 standard; protein; 395 AA. ID ABUS3160; XX AC ABUS3160; XX DT 14-APR-2003 (first entry) XX XX DT H	l; gene therapy; vaccine; disease treatment sapiens.
8.08e-16									ATCATCCGCAGGGC 748          : : :   ProProAlaSerTh 1514  ICCAGACAGGGGTC 808  ICCAGACAGGGGTC 818  I
	8.08e-16 Length: 5179 336.50 Matches: 141 11.8* Conservative: 55 Mismatches: 198 11.8* Indels: 190 9 Gaps: 22 (1-1561) x AEA27639 (1-5179)	LIST		eAsnGluAspHisProSerSerGlySerAspAspGlyAsp -TGTACCTTGCCGCAGAACGCGGCGTGCGCGTACGCC 	InHisGlyGlnLysValGlnCysAspValSerValGl)	-TGCTGTTGG	CCCTTGTCCTACGCAAATGGCGCGCACTCGGCTAC(		696GCTACTGGGCAAGCCATTCCGCCCACAACGCCACGCGCCCCCGCGCCCCCCCC

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                                                                                                                                                                                                                                                                      This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
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                                                                                                                                                                                         Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
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                18-AUG-2000;
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| HisAlaArgArgGInProAlaGly------466
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|ProGluArgArgGlnProArgProArgGlnArgArgGlnProArgArgArgArgGlnCys 454
AlaTyrArgTrpArgAlaGlyGlnProGlyArgProProGlyGlnProGlyArgGlnPro 140
                                                         ---GlnArgArgArgArg 153
                                                                                                                     ArgalaGlnGlnArgGlnGlyLeuAlaAspAlaGlyHisArgAlaValArgGlnGlnArg 173
                                                                                                                                                                                  ArgargHisProGlyAlaValAlaGlyAspSerArgArgAlaArgArgAlaGlnProAla 193
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| ArgProAlaThrGlyGlnProGlyGlnArgArgAhaHisProProHisArgGlnTrp 333
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                            CGAATCTGCCGAACACAGCCTCGATTTGCAATACTACATTTGGCGCAACGACATTTCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences AB067826-80804396. represent P. aeruginosa polypepitides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to Pseudomonas aeruginosa polypeptides and the polynuclectides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant components for allowed peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa caused infection, and in detection of P. aeruginosa sequences or other sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 AlaGlyArgGlnProdlyGlnProProGlyHisAlaProGlyProGlyArgGlnProAla 120
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                                                                                                                      Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
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ABO73174 standard; protein; 822
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                                                                                         Pseudomonas
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Human; gene therapy; vaccine; disease treatment; detection.

WO200112659-A2

18-AUG-2000; 18-AUG-1999;

22-FEB-2001

Human testes-derived DKFZphtes3\_2a11 homologue #19

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1167
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1039 AGACGCACTGGCAAAACTGGTGCAGGACGGCATAGACGTTACCGTCCTGACCAACTCGCT 1098
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(GEHU-) GERMAN HUMAN GENOME PROJECT,

WPI; 2001-327840/34.

99US-0156503P

28-SEP-1999;

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from human cDNA libraries which can be used for gene therapy or in vaccines. The polymucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
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protein; 386 AA

standard;

ABU53159 ABU53159 14-APR-2003 (first entry)

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CCGCGTTACCCTCGACAAACACAAACGCCTGCAATGGCACGATCCCCGCCACCCGGAAAAAC 1479
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         ---ThrProSerProProThrThrMetT 345
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                                                               hrThrLeuProProThrThrSerSerProLeuThrThrProLeuProProSerI
                                                                                           1480 CTACCCGAACGAACCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATCCTATCCCT
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106 ACTGGAAGAACGGACGGAAAGC	268 ATCTGCCGAACACGCCTCGAI 65 hr	448 TATCGAAGTGCGCTGTTCAACC 113 leThrProProAlaSerThrThrThrLeu 499 CGGCTACCTGACGACTTCCCCGGCTCA 127 hrProSerProProThrThrThrThrThrThr 559 CGACAACCGCGCCACCATAC 559 CGACAACCGCGCCACCATAC 57 roThrThrPro11eThrProProProThr	610 CAAAGTCGGTGAGGACACCGT7 167 roSerPro 670 CGGCGAAGTATCGCACGACTTC ::	202	904 CGACACCTGCAAAAGGACTC
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XX SQ Sequence 387 AA;	
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US-10-665-990A-13 (1-1561) x ABU53161 (1-387)	268
QY 46 ACGCAGCCTCATTTCCCTTTTATGCCTCCTTCTTCTTCATGTTCTTCATGGTTGCCCC 105	OY 1084 CCTGACCAACTGGCACGACGTTGCCGCGTCCATTCCGGCTACGTCAAATA 1143
OY 106 ACTGGAAGAACGGACGGAAAGCCGTCATTCAATACTTCCAAACCTGTCCTGGACAA 165	Qy 1144 CCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCAACCA 1197
	Qy 1198 TGCCGTCCCGCCAAAAGACAAAGGCTGACGGCAGCTCCGTAACCAGCTTGCATGC 1257
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3GCAG	Qy 1318 TTCCGCACGGCTCAATACCGAAATGGGCGTCGTCATCGAAAGCCCCAAAATCGCAGAACA 1377
GCTGCTGTTCAACCTCATGTACCTTGCGCAGAACGCGGCGCGCGC	OY 1378 GATGGAGCGCACCTCGCCGATACCACCCGAATACGCCTACCGCGTTACCCTCGACAA 1437
GGACGACAACAACACGCGGGGTTGGACGATCTCCTGCTCGCCCTCGACAGCCATCCCAA	Qy 1438 ACACAACGCCTGCAATGGCACCGCCACCCGAAAAACCTACC 1484
CACT	SUL 353
Qy 499 CGGCTACCTGACCGACCTCCCCGCCTCAACCGCCGCATGCACAAATCCTTTACCGC 558	AC ABU53157; XX DT 14-APR-2003 (first entry) XX
Qy 559 CGACAACCGCGCCACCATACTCGGCGGACGCAATATCGGGACGACGAATACTT 609	DE Human testes-derived DKFZphtes3_2all homologue #17. XX XW Human; gene therapy; vaccine; disease treatment; detection. XX
Qy 610 CAAAGTCGGTGAGGACACCGTTTTCGCCGACGTGGACATCCTCGCCACCGGCAGCGTCGT 669  182 roSerPro	OS Homo sapiens. XX PN WO200112659-A2. XX
Qy 670 CGGCGAAGTATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAAGGCCAC 729 1:	22-FEB-2001. 18-AUG-2000; 20
Oy 730 GCGCATCATCCGCAGCGGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGA 789	
790 AACATCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAAA	FA (GENU-) GEKMAN HUMAN GENOME PROJECT. XX PI Wiemann S;
Db 222 roSerProProThrThrThrThrThrThrProProProThrThrProSerProProT 242	XX DR WPI; 2001-327840/34.
OY 844 CTACCAAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTGATCAG 903 	
	PS Example III; Page 773-774; 1095pp; English.

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CCCCAAAATCGCAGAACAGATGGAGCGCACCCTCGCCGATACCACACCCGAATACGCCTA 1419
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            This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and tratment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity, the antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
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                                                              The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
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New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused b. aureus, e.g. sepsis.
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                                                                                     ProThrLysValSerArgHisAlaSerSerSerProGluSerProLysProAlaProAla
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                                                                                                                                                                                                                                                                                                                            The invention relates to forming (M1) an isolated ribonucleoprotein (RNP) complex (C), involves contacting an RNA affinity substrate (S) comprising C an RNP assembly sequence (AS) and an affinity rag, with a protein mixture to permit formation of (C) on AS, subjecting (C) to chromatographic c separation, and subjecting (C) to affinity selection, where the affinity c tag (e.g. bacteriophage MS2 coat protein in a fusion protein with E. coli malcose binding protein) binds to an affinity matrix. Also included are an isolated spliceosome preparation (isolated by (M1)), a RNA comprising an ENP complex binding site and at least one phage coat protein cracognition site, a nucleic acid encoding the RNA, and treating (M2) a subject having a disorder associated with abnormal RNP complexes (by obtaining a sample of cells from a subject, purifying RNP complexes (by obtaining a sample of cells from a subject, purifying RNP complexes (by complex selected from a subject. (M1) determining the presence in the complex selected from a spliceosomal complex, and normalising the amount of RNPs in the subject. (M1) is useful for forming an isolated RNP complex, an mRNA export complex, or an H complex. (M1) is useful for forming an isolated RNP complex, an mix and adagnostic assay for determining whether a subject has abnormal RNP complexes (M2) is useful for treating a subject has a disorder associated with abnormal RNP complexes. (M2) is useful for treating a subject has a complex. The present sequence represents a putative novel human complex. The present sequence represents a putative novel human complex. In the present sequence is not shown in the specification complex. In the specification of the specification is solved the information provided in table 2 of the specification.
                                                                                                                                                                                                                               Isolating ribonucleoprotein complex, by contacting RNA affinity substrate having ribonucleoprotein assembly sequence and affinity tag, with protein mixture, subjecting complex formed to chromatography, affinity selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 AACACGCAGCCTCATTTCCCTTTTATGCCTCCTTCTCTGTTCATGTTCTTCATGGTTGCC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---AlaGluArgHisGlyGlySerPro----GlnProLeuAlaThrThrProLeuSer 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 CTACCTGCTCGACGACCC-------------------CCACGAAGCCCTTGCCGC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 CCCACTGGAAGAACGGACGGAAAGCCGTCATTTCAATACTTCCAAACCTGTCCTCCTGGA
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Matches:
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                                                                                                                                                                                                                                                                                                  Claim 24; Page; 39pp; English
                                    14-JAN-2002; 2002US-00047991
                                                                       12-JAN-2001; 2001US-0261521P
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37.6%
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Query Match:
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us-10-665-990a-13.rag

PA (RIGE-) RIGEL PHARM INC.  XX  PI Lorens JB, Atchison RE, Friera A, Holland S;  XX  DR  W-PSDB; ADN60279.  XI Identifying a compound that modulates angiogenesis or tumorigenesis, useful in diagnosing and treating angiogenesis, cancer, stroke, infertility and heart disease, comprises contacting the compound with angiogenesis polypeptide.  XX  PT  Magiogenesis polypeptide.  XX  XX  Disclosure; Page 70-71; 105pp; English.  XX  CThe present invention describes a method for identifying a compound that	CC modulates anglogenesis or tumourigenesis. The method comprises: (a) contacting the compound with anglogenesis polypeptide, e.g. Ax1, tubulin coffector D. transglutaminase 2, cytosine deaminase, peptidase M41 confector D. transglutaminase 2, cytosine deaminase, peptidase M41 cc (paraplegin), CD13 aminopeptidase, PPK-1, zip kinase, Gas6, SRm160, non-semblorin, novel zinc finger helicase (FLU2261), plexin-A2, cc deoxycytidylate deaminase or novel sugar transporter, novel cunctional effector of the compound upon the anglogenesis polypeptide or the physical effect of the compound upon the target polypeptide or its fragment or inactive variant; and (c) determining the chemical or compound that modulates cell comprising the chemical or compound that modulates cell cycle arrest. Also described is a method of condulating anglogenesis in a subject. The anglogenesis or tumourigenesis condulating compound has antianglogenic, cytostatic, cerebroprotective, vasotropic, antiherility and cardiant activities, and can be used in antibody, antisense and RNA interference (RNA) therapies. The methods and compounds or compositions are useful in diagnosing and treating cuptenese text and compound that modulates anglogenesis. The methods and compounds or compositions are useful in diagnosing and treating cyclence represents a human splicing coactivator submit SRm300 protein, which is used in the exemplification of the present invention.	Alignment Scores: 1.79e-13 Length: 2296 Pred. No.: 303.50 Matches: 156 Score: 37.6% Conservative: 78 Best Local Similarity: 25.1% Mismatches: 23 Query Match: 10.6% Indels: 156 DB: 8 Gaps: 29 US-10-665-990A-13 (1-1561) x ADN60280 (1-2296)	Qy 43 AACACGAGCCTCATTTCCCTTTTATGCCTCCTTCTGTTCATGGTTGCC 102  :::	Oy 214 CTACCTGCTCGACGACCC 249
Db   715 LysLysSerArg1leSerSerArgSerArgSerLeuSerSerProArgSerLysAla 734     Qy		905 SULT 33 N60280 ADN60280 ADN60280;	Human splicing coactivator subunit SRm300 protein.  XX  XX  XX  XM  Angiogenesis modulator; tumourigenesis modulator; angiogenesis; Ax1;  KW  tubulin cofactor D; transglutaminase 2; cytosine deaminase;  KW  peptidase M41; paraplegin, CD13 aminopeptidase; PPK-1; zip kinase; Gas6;  KM  SRm160; non-muscle myosin heavy chain; calmodulin 2; symporter;  KW  SRm160; non-muscle myosin heavy chain; calmodulin 2; symporter;  KW  SRm160; non-muscle myosin heavy chain; calmodulin 2; symporter;  KW  SRm160; non-muscle myosin heavy chain; calmodulin 2; symporter;  KW  SRm160; non-muscle myosin heavy chain; antiangiogenic; cytostatic;  KW  Antibody therapy; antisense therapy; RNA interference therapy;  KW  RNAi therapy; cancer; stroke; infertility; heart disease; human.	OS Homo sapiens.  XX  XX  XX  PN W02004039955-A2.  XX  PD 13-MAY-2004.  XX  XX  XX  XX  XX  XX  XX  XX  XX

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invention describes a method for identifying a compound that ngiogenesis. The method comprises: (a) the compound with angiogenesis polypeptide, e.g. Ax1, tubulin transglutaminase 2, cytosine deaminase, peptidase M41.

Langulutaminase 2, cytosine deaminase, peptidase M41.

Langulutaminase 2, cytosine deaminase, peptidase M41.

Langulutaminase 2, cytosine deaminase, peptidase M41.

In heavy chain, calmodulin 2, novel symporter, novel novel zinc finger helicase (FLJ22611), plaxin-A2.

Iate deaminase or novel sugar transporter; (b) determining the effector of the compound upon the angiogenesis polypeptide or its inactive variant; and (c) determining the chemical or effect of the compound upon a cell comprising the target or its inactive variant; and (c) determining the chemical or effect of the compound upon a cell comprising the target or its in modulates cell cycle arrest. Also described is a method of angiogenesis in a subject. The angiogenesis or tumourigenesis antimicrility and cardiant activities, and can be used in attience and RNA interference (RNA) therapies. The methods antisense and RNA interference (RNA) therapies. The methods should be an unit of angiogenesis. The methods is concern, stroke, infertility and heart disease. The present presents a human splicing coactivator subunit SRM300 protein, and in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| |||||||
proValAsnProProSerGluAlaSerProThrArgAspArgSerProProLys 407
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   Friera A, Holland S;
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8 % 8 6 6 6 6 6 6 යි රි The present invention describes a method for identifying a compound that modulates angiogenesis or tumourigenesis. The method comprises: (a) contacting the compound with angiogenesis polypeptide. e.g. Ax1, tubulin confactor D, transglutaminase 2, cytosine deaminase, gas6, SRm160, non-muscle myosin heavy chain, calmedulin 2, novel symporter, novel coffered and neavy chain, calmedulin 2, novel symporter, novel compound upon the angiogenesis polypeptide or compound upon the angiogenesis polypeptide or the physical effect of the compound upon the angiogenesis polypeptide or transporter in active variant; and (c) determining the chamical or the physical effect of the compound upon the angiogenesis polypeptide or transporter in active variant; and (c) determining the chamical or phenotypic effect of the compound upon a cell comprising the target polypeptide or its fragment or inactive variant, thus identifying a compound that modulates cell cycle arrest. Also described is a method of modulating angiogenesis in a subject. The angiogenesis or tumourigenesis compound that modulates and RNA innerference (RNAi) therapies. The methods and compounds or compositions are useful in dientifying a compound that modulates angiogenesis. The methods and compounds or compositions are useful in dientifying a compound that modulates angiogenesis. The methods and compounds or compositions are useful in dientifying angiogenesis, cancer, stroke, infertility and heart disease. The present sequence represents a human serine/arginine repetitive matrix 2 protein, which is used in the exemplification of the present invention. Disclosure; Page 68; 105pp; English. angiogenesis polypeptide. 

Sequence 2752 AA;

Scores: 1.87e-13 Length: 2752 303.50 Matches: 156 milarity: 37.6\$ Conservative: 78 Similarity: 25.1\$ Mismatches: 233 h: 10.6\$ Indels: 156 Gaps: 29	AACACGCAGCCTCATTTCCCTTTTTATGCCTCCTTCTCTGTTCATGTTCTTCATGGTTGCC :::	CCCACTGGAAACGGAAAGCCGTCATTCAATACTTCCAAACCTGTCCTCGGA	CAACATCCTGCAAATCCGGCACACCCCTCATAACAACGGGCTATCCGACAT	CTACCTGCTCGACGACCC	CCGCGCCCCCTTATCGAATCTGCCGAACACAGCCTCGATTTGCAATACTACATTTGGCG	CAACGACATTTCCGGCAGGCTGCTGTTCAACCT		CCTGCTGTTGGACGACACACACGCGCGGTTGGACGATCTCCT	GCTCGCCCTCGACAGCCATCCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCTACG
res: urity: nilarity: \-13 (1-1	AACACGCA:::    SerThrGl		CAACATCC				AlaLysArg	CCTGCTGT        ProAlaTh	GCTCGCCC
Alignment Scores: Pred. No.: Score: Score: Score: Store Similarity: Best Local Similarity Query Match: DB: US-10-665-990A-13 (1-:	43	103	163	214	250	310	343	379	424
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249 426 309 446 342 466 378 486 423 505 483 · ;

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qq	:::	520
S S	484 CAAATGGCGCACTCGGCTACCTGACCGACTTCCCCGGCTCAACCGCCGCATGCACAA :::	543
cy G	544 CAAATCCTTTACCGCCGACAACCGCGCCACATACTCGGCGACGAATATCGGCGACGA 	603
ò t	ATACTTCAAAGT	663
8 8	554 SerArgSerAlaArgArgGlyArgSerHisSerArgSerFroAlaThrArgGlyArgSer 664 CGTCGTCGGCGAAGTATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCGACAAA	573
7 A		593
'n	724 CGCCACGCATCCACACAGCAACAT	762
qq	rgArgSerArgSerArgThrProAlaArgArgGG	613
b Q	763 TCTTCAAGCACTCGGATACAACGACGAAACATCCAGACACGCGCTCCTGCGCTACCG	819
δ	0 CGAAACCGTCGAACAGTCGCCCTCTACCAAAAAATACAGACG	879
qq	633 ArgargSerArgSerArgSerProAlaArgArgSerGlyArgSerArgSerArgThrPro	652
λo	80 GAGGGCCAAACCCGCCTGATCAGCGACACCCCTGCAAA	933
qq	3 AlaArgArgGlyArgSerArgSerArgThrProAlaArgArgGlyArgSerArgserAr	672
જે ત	4 CCGCCGCAAACCGCCGATTGCCGGGAGGCTGCAAGA	9
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g qq		1 0
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qq	732AsnLysSerArgThrSerGlnArgArgSerArgSerAsnSerProGluMet	749
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qq	750 LysLysSerArglleSerSerArgArgSerArgSerLeuSerSerProArgSerLysAla	169
ර ර	1159 CAAAGCCGGCATCAAACTCTACGAGCTGCAACCAACCATGCCGTCCCGGCAC	1212
3 8	13 ababanababananangan Propertional arabanangan sa sa sa sa sa sa sa sa sa sa sa sa sa	0
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λ̈́o	1254ATGCCAAAAQCTTCATTGTGGACGCCA	1280
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ò	1281 AACGCATCTTCATCGGCTCATTCAACCTCGACCCCCGTTCCG	1322
qq	829 ThrProSerArgGlnSerHisSerSerSerSerProHisProLysValLysSerGlyThr	848
<b>۸</b> ٥	1323CACGGCTCAATACCGAAATGGGCGTCGTCATCGAAAAGCCCCAAAATCGCAG	1373

370 162

thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous cystem, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary complianty cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's circlease, an autoimmune or immune-mediated skin disease, a bullous skin disease, asthma, allergic rhinitis, atopic dermatitis, psoriasis, an allergic contact dermatitis, psoriasis, an allergic contact dermatitis, food controphilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity, urticaria, an immunologic disease of the lung, confined the invention.  CC graft-versus host disease. The present sequence represents a PRO protein cc the invention.  XX Sequence 2752 AA;	Alignment Scores:  Pred. No.:  Pred. No.:  303.50  Matches:  Score:  Percent Similarity:  Best Local Similarity:  10.6\$  Mismatches:  233  Query Match:  8  US-10-665-990A-13 (1-1561) x ADP24102 (1-2752)	ACGCAGCCTCATTTCCCTTTTATGCCTCCTTCTCTTCATGTTGCTTGC	Qy         103 CCCACTGGAAGAACGGAAAGCCGTCATTTCAATACTTCCAAACCTGTCCTCCTGGA 162	Qy 214 CTACCTGGACGACCA	Qy 250 CCGCGCCCTTATCGAATCTGCCGAACACAGCCTCGATTTGCAATACTACATTTGGCG 309	Db 447 ProGlySerHisArgGluIleSerSerSerProThrSerLysAsnArgSerHisGlyArg 466  Qy 343	379 CCTGCTGGACGACAACAACACGCGCGGGTTGGACGATCTCCT	Oy 424 GCTCGCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCTACG 483	Qy 544 CAAATCCTTTACCGCCGACAACCGCGCCCATACTCGGCGACGCAATATCGGCGACGA 603 :::
Db 849 ProProArgGlnGlySerIleThrSerProGlnAlaAsnGluGlnSerValThrProGln 868  1374 AACAGATGGAGCGCACCCTGGCGATACCACCCGAATACGCGTTACCCTG 1433	Qy       1551 AAGGTT 1556         :::           :::            Db       940 Argval 941         RESULT 35       ADP24102         ID       ADP24102 standard; protein; 2752 AA.         AC       ADP24102;		<pre>KW osteopathic; antidiabetic; dermatological; antirheumatic; immunosuppressive; KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system. XX OS Unidentified. XX XX XX XX XX XX XX XX XX XX XX XX XX</pre>	XX PD 21-MAY-2004. XX PF 30-OCT-2003; 2003WO-US034312.	01- (GE	Wu TD; WPI; 2004-419628/39. N-PSDB; ADP24101. New DPO nolymerides and nolymicleotides useful for treat	region of the state of the stat	PS Claim 7; SEQ ID NO 1280; 2940pp; English.  XX CC The invention relates to a novel isolated nucleic acid and the PRO CC polypeptide encoded by it. A protein of the invention has CC antiinflammatory, antiarthritic, antiinflammatory, antiarthritic, antipeoralic, intipsoriatic, antiallergic, costeopathic, antidiabetic dermacological, antipsoriatic, antiallergic CC antiasthmatic, hepatotropic, and respiratory activity. A polymucleotide CC of the invention may have a use in gene therapy. The PRO polypeptide, its	

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1000 -----TCTGGTTTCACCCTATTTCGTCCCTACAAAATCCGGCACAGACGCACTGGC 1050
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| Pro-----AspProdlyGluArgArgHisAlaGluGlnGlyArgArgGlyValGlyGln 376
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ProAspArgHisArgGlnProArgArgPheArgProArgArgProValGluLeuGlyGly 396
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                                                                                        ----GlyHis-----ArgProGly
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                                                                                                                                          CATCCTCGCCACCGGCAGCGTCGTCGGCGAAGTATCGCACGACCTTCGACCGCTACTGGGC
                                                                                                                                                                         CACGCGCATCATCCGCAGCGGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 ArgProGluProAlaAlaAspGluArgGluGluGluArgArgArgAlaValLeuGlyArg
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559 ThrargHisArgGlyGlnGlyAsnAlaThrLeuArgLeuProLeuAlaLeuLeuArgArg
                                 ACGCAATATCGGCGACGAATACTTCAAAGTCGGTGAGGACACCGTTTTCGCCGACCTGGA
                                                                                                                                                                                                                                                                                                  ArgAlaArgArgArgProAlaProAlaAspArgArgAlaGlyTrpGlnGlyProGlyArg
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                                                                                                                                                                                                                                                                                                                                    The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therefore therapy of pathological conditions resulting from a prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, or the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. reartment of P. aeruginosa-caused infection, and in detection of P. reartment of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this parent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                 Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
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1068

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------GlyArgGlnArg

DB: Gape: 38 US-10-665-990A-13 (1-1561) x ABO74950 (1-618)	Qy 169 CCTGCAAATCCGGCACACCCTCATAACAACGGGCTATCCGACACTTACCTGCTCGACGA 228	Qy 229CCCCCACGAAGCCCTTGCCGCCGCCGCCGCTTATCGAATCTGCCGAACA 279	280 CAGCCTCGATTTGCAATTTGGCGCAACGACAT3	DD 43	:::       TrpbrodlyAlaProAlaAlaMetGlyLeuArgArgAlaTrpbroAla 73	Qy 346 GTACCTTGCCGCAGAACGCGGCGTGCGCGTACGCCTGTTGGACGACAACAACACGCG 405	Db 74 AlaProCysGlyArgArgArgArgAroAspThrGlnLeuArgLeu 88	69 AEGNOCHIMIGGINSEKGIYAEGARIGINEKOAARAKIOKAT	104 ArgProGlnProGlyLeuArgCysProArgProAlaGlyArgProGluArgSerProArg	Qy 496 ACTCGGCTACCTGACCGACTTCCCCGCCTCAACGCGCACGAACAA 546	Db 124 ArgGlnAspProThrArgLeuArgArgProGlyGlnProHisArgGlyGlnGlyProAla 143	547ATCCTTTACGGCGACAACCG	DD 144 AEGCYBHISHISHYOLEUAIGILEAIGAIGFIOALGGINFYOARGFIOINKOIYGINFIO LES Qy 568ÇGCÇAÇÇAÇÇATACTCGGÇGAACGAATATÇGGÇGACGAATACTTÇAAAGTCGGTGA 621		Qy 622 GGACACCGTTTCGCCGACCTGGACATCCTCGCCACCGGCAGCGTCGTCGCAAGTATC 681	Db 181 ProHisArgArgSerArgCysGlyHisArgValSerLeuArgArgProGlnSerAla 199	Qy 682 GCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAACGCCACGCGCATCTCCG 741	Qy 742 CAGCGGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAAACATCCAG 798	23		ACCCGCCTGATCAGCGACACCCCTGCAAA	246	Qy 919 AGGACTCGACCGCGCAAACCGCCGATTGCCGGGAGGCTGCAAGACGCGCT 975	Db 258ProArgProAlaAspProAlaArgProArgAspLeuProLeuArgArgGly 274	Qy 976 CAAACAGCCCGAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCCTACAAAATCCGG 1035	GinProThrAlaGlyAspArgLeuProLeuArgProArg	Qy 1036 CACAGACGCACTGGCAAAACTGGTGCAGGACGG 1068
Qy 1423	Qy 1462 TCCGGCCACCGGAAAAACCTACCGGAACGAACCGAAGCCAAACTTGGAAACGCATCG 1521	Qy 1522 CGCAAAAATCCTATCCCTGCTGCCCATCGA 1551	,	ABO74950;	XX DT 29-JUL-2004 (first entry)	XX DE Pseudomonas aeruginosa polypeptide #7125. XX	 XX	EN US0331/33-B1. XX 20 33. NDB-2003		XX PR 18-FEB-1998; 98US-0074788P. PR 27-JUL-1998; 98US-0094130P.	(GENO-) GENOME	Rubenfield MJ, Nolling J,	AX WPI; 2003-615309/58. DR N-PSDB; ABD08521.	Novel isolated nucleic	userui as molecurai cargets lor diagnostics, prophylaxis and treatment pathological conditions resulting from bacterial infection.	PS Disclosure; SEQ ID NO 23696; 455pp; English.	AA. C. The invention relates to Pseudomonas aeruginosa polypeptides and the C. polynucleotides encoding them. The sequences are useful in diagnosis and C. therapy of pathological conditions, as molecular targets for diagnostics,			CC production of P. aeruginosa-derived peptides or polypeptides, as target CC components for diagnosis and/or treatment of P. aeruginosa-caused				SQ Sequence bls AA;	1.68e-13 Length: 302.00 Matches:	larity: 34.8% imilarity: 29.0%	10.6% Indels:

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1272
                                                                                                         -----GGCGACCGACGTTGCCGCCGTCCATTCCGGCTACGTCAA---ATACCGAAA 1149
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                                                                                                                             328 ProAspLeuGlyGlnArgHisHisSerGlnPro---ArgValArgProGlyLeuProThr 346
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347 AlaAlaGluGlyArgProLeuAlaGluArgLeuProAlaArgCysGlnTrpGlnTyr 366
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------ProAspArgGlyThrArgArgProGlyArgAlaGlnLeuCysLeuArgArg
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                                                 GACCAACTCGCTACA--
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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with alternation intervention. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial composition acidosis and stroke (MERRP), mycolonic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387
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                                                                                                                                                                                                                                                              Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 CCCACTGGAAGAACGGACGGAAAGCCGTCATTTCAATACTTCCAAACCTGTCCTCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        371 ---AlaGluArgHisGlyGlySerPro----GlnProLeuAlaThrThrProLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 CAACATCCTGCAAATCCG-----GCACACCCCTCATAACAACGGGCTATCCGACAT
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                                                                                                                                                                                  Glenn
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2231; 180pp; English.
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                                                              2002US-0372843P.
2002US-0389987P.
2002US-0412418P.
                                04-APR-2003; 2003WO-US010870.
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Best Local Similarity:
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                                                              12-APR-2002;
17-JUN-2002;
20-SEP-2002;
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23-OCT-2003
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Warnock DE;
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as a polype as compon bacterial of recombinan peptides, a ginosa caus nences Aboe inneces Aboe inneces aboe		Alignment Scores:	1.99e-13 Length: 301.00 Matches:	Percent Similarity: 34.6% Conservative: 31 Best Local Similarity: 29.4% Mismatches: 196	Toos indels:	US-10-665-990A-13 (1-1561) x ABO79612 (1-618)	Qy 169 CCTGCAAATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACGA 228		Qy 229CCCCCCCCCCTTGCCGCCCCCTATCGAATCTGCAACA 279		Qy 280 CAGCCTCGATTTGCAATACTACATTTGGCGCAACGACAT318	Db 43HisGlnGlyGlnSerHisArgProAlaHisGlnGlyArg 55	Qy 319319		Qy 346 GTACCTTGCCGCAGAACGCGGGGTGCGCGTACGCCTGCTGGTGGACGACAACAACAACAACGGG 405		Qy 406 CGGGTTGGACGATCTCCTGCCTCGACGACCATCCCAATATCGAAGTGCGCCTGTT 465	Db 89 ArgProGlnArgGlnSerGlyArgArgAsnGlnProAlaProVal 103	Oy 466 CAACCCTT	Db 104 ArgProGlnProGlyLeuArgArgProArgProAlaGlyArgProGluArgSerProArg 123	496		547	Db 144 ArgArgHisHisProLeuArgİleArgArgProArgGlnProAspProThrGlyGlnPro 163	QY 568CGCCACCATACTCGGCGACGAATATCGGCGACGAATACTTCAAAGTCGGTGA 621	Db 164 GlyGlnArgHisHisLeuArgAlaArgArgArgArgGlnArgHisPro 180	QY 622 GGACACCGTTTTCGCCGACTGGACATCCTCGCCACCGGCAGCGTCGTCGGCGAAGTATC 681	Db 181 ProHisArgArgSerArgCysGlyHisArgValSerLeuArgArgProGlnSerAla 199	ACTGGGCAAGCCATTCCGCC	Db 200 GlyArgAlaProLeuAlaGluArgProGluProArgArgThrValPro 215

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ò	742 CAGCGGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAACATCCAGACA 801
Ор	
ò	802 CGCGCTCCTGCGCGTACCGCGGAAACCGTCGAACAGTCGCCCCTCTACCAAAAATACAGAC 861
. Qa	227 ArgProProGlyArgHisArgArgCysProArgGlnProGly 240
δ	92
ηΩ	241 ValProLeuArgArgAlaArgGlnProGlyArgAlaGlyThrGlnHisPro 257
ò	97
qq	
ò	979 ACAGCCCGAAAAAAGGTCTATCTGGTTTCACCCTATTTCGTCCTACAAAATCCGGGAC 1038
qq	276 ProThrAlaGlyAspArgLeu
δλ	1039AGACGCACTGGCAAAACTGGTGCAGACGGCAT 1071
QQ	289 ArgLeuProAlaGlnArgArgArgProGlyArgGlnArgAspProGlySerGlyArgGln 308
δ	1072 AGACGTTACCGTCCT101
q	309 GlyAlaGluHisProGlyTrpAlaAspArgLeuProAlaLeuArgProAlaAlaAlaPro 328
ò	1102GGCGACCGACGTTGCCGCCGTTCCCGCTACGTCAAATACCGAAAACC 1152
q	329 AspLeuGlyGlnArgHisHisSerGlnProArgValArgProGlyLeuProThrAla 347
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qq	   ProLeuAlaGluArgLeuProAlaArgCysGlnTrpGlnTyr
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qa	405 ArgGlnProHisProThrGlnArgGlnProArgLeuArgArgHisArgGlnGlnPro 423
ò	1309 CGACCCCGTTCCGCACGCTCAATACCGAAATGGGCGTCGTCATCGAAAG 1359
QQ	424 GlyLeubroValArgAlaArgGlnGlnProlleAspArgHisArgArgAlaSerGlyAsp 443
δ	1360 CCCCAAAATCGCAGAACAGATGGAGCGCACCCTCGCCGATACCACCCGAATACGCCTA 1419
ΩÞ	444 GlnArgArgArgGlnProHisProGlyProArgArgAlaGlnThrGlyLeuArgArg 463
ζ	1420 CCGCGTTACCCTCGACAACAACGCCCTGCAATGGCA
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δ	1459CGA 1461
Ωp	484 ArgProArgProAlaHisArgGlnAlaHisProArgGluHisHisHisLeuProLeuArg 503
δλ	1462 TCCCGCCACCCGAAAAACCTACCCGAACGAAACCCGAAACTTTGGAAACGCATCGC 1521
Ωp	504 SerArgArgProValAlaArgArgSerArgThrArgArgGlnArgProGluThrAlaSer 523
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2, 2006, 05:52:55 ; Search time 49.2 Seconds Мау Run on:

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2651.348 Million cell updates/sec

US-10-665-990A-13 2852 1 caaaatacaggcaatgccgt......tgcccatcgaaggtttatta 1561 Title: Perfect score: Sequence:

**BLOSUM62** Scoring table:

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3735138 Total number of hits satisfying chosen parameters:

1867569 segs, 417829326 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 14, Appl	Sequence 16, Appl	18,		Sequence 4, Appli	20.		9086		Sequence 9084, Ap	Sequence 1068, Ap
ID	US-10-665-990A-14	US-10-665-990A-16	US-10-665-990A-18	US-10-066-551-4	US-10-665-990A-4	US-10-665-990A-20	US-10-335-977-9085	US-10-335-977-9086	US-09-881-752A-356	US-10-335-977-9084	US-09-922-217-1068
DB	ß	S	ß	4	Ŋ	'n	4	4	m	4	m
% Query Match Length DB	525	525	525	525	525	525	502	502	428	224	5179
% Query Match	94.3	94.0	93.9	92.2	92.2	92.2	22.2	22.2	20.7	12.6	11.8
Score	2689	2681	2677	2630	2630	2630	632	632	290	359	336.5
Result No.	н	7	e	4	2	9	7	80	6	10	11

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-263-106	-025-380-10	-10-734-564-1	09-801-368-10	-10-437-963-19	-10-696-909A-4	6-969-	10-408-765A-2	-09-840-7	10-437-963	-10-084-846A-	0-418-	-10-626-832-8	-10-437-963-17	10-437-963-1766	10-724-972A-3	-09-828-	-09-966-521-1	US-10-429-094-18	-09-828-523A-	09-966-521-8	-10-429-094-8	-10-084-846A-	-11-097-143-4	-10-684-42	-10-437-963-1994	-10-437-963-1	0-084-846A-	-10-335-977-	-11-097-143-3621	-10-437-963-1687	-10-450-763-5072	-10-437-963-2036	US-10-437-963-177697
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## ALIGNMENTS

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_	RESULT 1						
_	US-10-665-990A-14						
	Sequence 14. Application US/10665990A	ion US/10665990A					
	Publication No. US20040253222A1	4025322A1					
	GENERAL INFORMATION:						
	; APPLICANT: Apicella, Michael A.	Michael A.					
	; APPLICANT: Edwards,	Jennifer L.					
. ~		Vaccine and compositions for the prevention and	ositions for	the r	revention	and	treatme
	; TITLE OF INVENTION:	infections		•			
	; FILE REFERENCE: 17023-031001	3-031001					
. •	; CURRENT APPLICATION NUMBER: US/10/665,990A	NUMBER: US/10/66	5,990A				
	CURRENT FILING DATE: 2003-09-19	2003-09-19					
	; PRIOR APPLICATION NUMBER: US 10/621,184	MBER: US 10/621,	184				
	PRIOR FILING DATE: 2003-07-15	003-07-15					
	; PRIOR APPLICATION NU	APPLICATION NUMBER: US 10/066,551	551				
	PRIOR FILING DATE: 2002-01-31	002-01-31					
		APPLICATION NUMBER: US 60/344,452	452				
	; PRIOR FILING DATE: 2	2001-10-23					
		APPLICATION NUMBER: US 60/310,356	356				
-	PRIOR FILING DATE: 2001-08-06	001-08-06					
	PRIOR APPLICATION NUMBER: US 60/266,070	MBER: US 60/266,	070				
	PRIOR FILING DATE: 2001-01-31	001-01-31					
	NUMBER OF SEQ ID NOS: 32	: 32					
•	SOFTWARE: FastSEQ for Windows Version 4.0	r Windows Versio	n 4.0				
	SEQ ID NO 14						
•	LENGTH: 525						
	TYPE: PRT						
	ORGANISM: Neisseria gonorrhoeae 1291	gonorrhoeae 129	1				
	US-10-665-990A-14	ì					
7	Alignment Scores:						
	Pred. No.:	6.86e-172	Length:	525			
U)	Score:		Matches:	520	_		
щ	Percent Similarity:		Conservative:	0			
щ	Best Local Similarity:	100.0%	Mismatches:	0			

DB: US-10-665-9 US	1.1561  x US-10-665-990A-14 (1-525)	0.02   0.02
ठेत ठेत	902 AGCGACACCCTGCAAAAGGACTCGACCGCCGCAAACCGCCGATGCCGGGAGG 961 306 SerAspThrProAlaLySGlyLeuAspArgAspArgLySProProIleAlaGlyArg 325 305 CTGCAAGACGCCCTCAAACAGCCCGAAAAAAGCGTCTATTCGCTTTTCGCTCTTTTCGTC 1021 306 LeuGlnAspAlaLeuLySGlnProGluLySSerValTyrLeuValSerProTyrPheVal 345	Alignment Scores:  Pred. No.: 2.366-171 Length: 525 Score: 2681.00 Matches: 518 Percent Similarity: 99.8\$ Conservative: 1 Best Local Similarity: 99.6\$ Mismatches: 0 Ouery Match: 54.0\$ Indels: 0

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RESULT 3
US-10-665-990A-18
Sequence 18, Application US/10665990A
Sequence 18, Application US/10665990A
Sequence 18, Application US/10665990A
Sequence 18, Application No. US2004025322A1
GENERAL INFORMATION:
APPLICAMY: Apicella, Michael A.
TITLE OF INVENTION: Usecine and compositions for the prevention and treatment of Nell TITLE OF INVENTION: infections
TITLE OF INVENTION: infections
FILE REFERENCE: 17023-031001.
FILE REFERENCE: 17023-031001.
FRIOR APPLICATION NUMBER: US 10/665,590A
FRIOR APPLICATION NUMBER: US 10/666,551
FRIOR APPLICATION NUMBER: US 60/310,356
FRIOR FILING DATE: 2001-10-23
FRIOR APPLICATION NUMBER: US 60/266,070
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346. ProThrLysSerGlyThrAspAlaLeuAlaLysLeuValGlnAspGlyIleAspValThr 365
                                                                                                                                   TACCGAAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCAACCATGCC
                                                                                              386 TyrkrglysProLeuLysAladly1leLysLeuTyrdluLeuGlnProAsnHisAla
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Conservative:
Mismatches:
Indels:
Gaps:
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ORGANISM: Neisseria
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Best Local Similarity:
Query Match:
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RESULT 4

US-10-066-551-4

Sequence 4, Application US/10066551

Publication No. US20030100071A1

GENERAL INFORMATION:

APPLICANT: Apicella, M. A.

APPLICANT: Edwards, J. L.

APPLICANT: Edwards, J. L.

APPLICANT: Brown, B. W.

APPLICANT: Brown, B. W.

TITLE OF INVENTION: Vaccine and compositions for the
TITLE OF INVENTION: Prevention and treatment of Neisserial infections

FILE REFERENCE: 875.045US1

CURRENT APPLICATION NUMBER: US/10/066,551

CURRENT FILING DATE: 2002-01-31

PRIOR PLLING DATE: 2001-02-3

PRIOR PLLING DATE: 2001-02-3

PRIOR PLLING DATE: 2001-08-06

PRIOR PLLING DATE: 2001-01-31

NUMBER OF SEQ ID NOS: 12

SEQ ID NOS: 12

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GRAAGCCGTCATTTCAATACTTCCAAACCTGTCCTCTGGACAACATCCTGCAAA GLUSETATGH	146 LeuLeuAlaiJeuAspSerHisProAsnileGlüValArgieuPheAsnProPheValieu 165  482 CGCAAATGGCGCACTCGGCTACCTGACCGACTTCCCCCGCTCAACCGCCCATGCAC  116 ArgiysTrpArgAlaleuGlyTyrLeuThrAspPheProArgLeuAsnArgArgMetHis 185  542 AACAAATCCTTTACCGCGACAACCGCCACTACTCGGCGGACGCAATATCGCGAC  186 AsnLySSerPheThrAlaAspAsnArgGACACCATATTICLeuGlyGlyArgAsnIleGlyAsp 205  602 GAATACTTCAAAGTCGGTGACGACACCGTTTTCGCCGACCTCCTCCCCCCCC	CTCTACCAAAAATACAGAGGACGCATCGACGCAGAGCGTCCAAACCGCCTGATC 50 LeuTyrGlnLysIleGlnThrGlyArglleAspTrpGlnSerValGlnThrArgLeulle 30 AGCGACACCCCTGCAAAAGGATCGACGGCACGCGCAAACCGCCTGATC 90 AGCGACACCCCTGCAAAAGGATCGACGCGCACAACCGCGATCGCGGGGG 96 ACGAACAACGCCTCAAAAAAGCGTCGACGCGCAAACCGCTAATCCGGGAGG 96 BETATACGGCACAAAAAAAGCGTCTATCTGGTTTCACCTATTTCGTC 10 ACGAAAAACCGCACAAAAAAAGCGTCTATCTGGTTTCACCTATTTCGTC 10 ACGAAAAATCCGGCACAGACACTGGCAAAAACTGGTGCAGACGGCATACCTATTTCGTC 10 ACTACTAAAAATCCGGCACAGACACTGGCAAAAACTGGTGCAGACGCATACACTACTATTTCGTC 10 ACTACTAAAAATCCGGCACAGACACTGGCAAAAACTGGTGCAGACGCATACACTACTATTTCGTC 10 ACTACTAAAAATCCGGCACACGCACTGGCAAAAACTGGTGCAGACGCATACACTCGCTAAAAATTTTCGTC 10 ACTACTAAAAATCCGCACACGCACACGCACACCCACCACACACA
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|AlaThrGluGluGlyIleLeuIleHisGluLysAsnSerProAspThrSerPhePheLeu 487
315 LysAspSerValPheIleAlaSerSerTyrPheIleProGlyLysLysIleMetLysIle 334
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ThrAspAlalleValValTyrGlyAlaTrpGluArgTyrArgAsnLysLeuValArgMet
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| GlyalaAsnValTyrGlulleArgAsnAspPhePheAsnArgGlnIleLysGlyArg---
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
FELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCATCGCCGCAAAATCCTATCCCTGCTGCCC 1546
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FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 227-7400
TELEFAX: (617) 742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
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CONTROL 19247-30.

SEQUENCE 356, Application US/09881752A
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FREED NO. US20020115078 Harold
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FREED NO. US20020115078A16 Helicobacter Polypeptides
FILE OF INVENTION: Identification of Polynucleotides
FILE REFERENCE: 06132/041002
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            CTGCGCTACCGCGAAACGTCGCCCCTCTACCAA---AAAATACAGACGGA
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| AspLeuSerSerGlnVallleAlaLysGluLeuLeuAsnAlaAlaAsnArgGlyValLys 109
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244 GluileAlaLysLeuHisGluLysIleProIleSerAlaGluAspAlaAsnGluPheGlu 263
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30 IleSerTyrAspProTyrThrThrIleGlySerLeuTyrAlaLysAsnLeuLysGlu
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...502
SEQUENCE DESCRIPTION: SEQ ID NO: 9086:
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                                                                                                                                                                                     ORGANISM: Helicobacter pylori
INFORMATION FOR SEQ ID NO: 9086:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                      6.25e-34
632.00
51.7%
32.8%
22.2%
                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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1148 AAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCAACCATGCCGTCCCC 1207
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LysLysMetMetLysIlePheLysAsnGlnIleSerLysGlyIleGluLeuAsnIleLeu 274
                                                        ACCAACTCGCTACAGGCGACCGTGCCGCCGTCCATTCCGGCTACGTCAAATACCGA
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IleAsnThrGluSerAlaValLeuPheAspAsnProSerPheAlaLysArgVal----
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: RUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compacible
COMPUTER: IBM PC Compacible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
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FILING DATE: 17-DEC-1997
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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INFORMATION FOR SEQ ID NO: 9084:
SEQUENCE CHARACTERISTICS:
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US-10-335-977-9084
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58 HisLysAsnIleGluValLysIlePheAsnProTyrTyrIleArgAsn---LysGlyLeu
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                                                                                                                                Conservative:
Mismatches:
Indels:
                                                                                                   Length:
Matches:
                                                                                                                                                                                    Gaps:
                 ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-356
                                                                                            3.99e-31
590.00
50.1%
32.3%
                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
 LENGTH: 428
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1387 nCysCysTrpProMetAspLysCysIleThrThrProSerProProThrThrProSe 1407
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1423 ----SerProProThrThrThrThrThrProProProThrThrThrProSerProPr 1441
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APPLICANT: Jiang, Yuqiu
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Mang, Aiun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OC COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT APPLICATION NUMBER: U1244
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
SEMOTH. 5179
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Matches:
Conservative:
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Indels:
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: Homo
US-09-922-217-1068
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Pred. No.:
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                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                          NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...224
SEQUENCE DESCRIPTION: SEQ ID NO: 9084:
                                                               ORGANISM: Helicobacter pylori
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Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
                                                                                                                                                                                     1.12e-15
359.00
59.1%
42.0%
                MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
 TOPOLOGY: linear
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Best Local Similarity:
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US-09-922-217-1068
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Pred. No.:
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                                                                                                                                                                     FOR THEIR
                                                                                             APPLICANT: Wang, Ajun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TGTACCTTGCCGCAGAACGCGGCGTGCGCGTACGCC---
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                     ; Sequence 1068, Application US/09833263; Patent No. US20020110547A1; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-833-263-1068
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-833-263-1068
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APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 1092213.0
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR PELICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
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Matches:
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Patent No. US20020128250A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
SEQ ID NO 108
LENGTH: 1367
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
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Best Local Similarity:
Query Match:
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CysThrLysGluLysProThrProThrThrSerCysThrLysGluLysProThr 28 GAAAGCCGTCATTTCAATACTTCCAAACCTGTCCTGGACAACTCTGCAAATCCGG 18 ProProHisHisAspThrThr-ProCysThrLysLysLysThrThrTsrLysGruThrCy 30 CACACCCCTCATAACACGGGCTATCCGAATTCTGTGTGACGACGACGAAGCC 24	242 CTTGCGGCGGGCGCTTATCGAAGAGCTGGTGATTTGCAA 295  126 ralaProValProThrProSerSerSerThrThrGluserSerSerAlaProValThrSe 346  296 TACTACATTTGGGGAACACATTTCCGGCAGGCTGCTGTTCAACCTCATGTACCTTGCC 355  11::	GATCTCCTGCTCGCCTCGACAGCCATCCCATATCGAAGTGCGCCTGTTCAACCCTTC	424 rSerThrThrGluSerSerAlaProValThrSerSerThrThrGluSerSerSerAl 444  584 GGACGCAATATCGGCGACGAATACTTCAAAGTCGGTGAGGACACCGTTTTCG 635	636CCGACCTGGACATCCTCGCCACCGCAGCGTCGTCGGCGAAGTATCGCACGACCTTC 691	770 GCAC	584 roserserserThrThrGluSerserAlaProValProThrProSerserSerThrT 604 911 CCTGCAAAGGACTCGACCGCCGCAAACGACTGCGGGAGGCTGCAAGAC 970 604 hrGluSerSerAlaProAlaProThrProSerSerSerThrThrGluSerSerSerA 624 971 GCGCTCAAACAGCCCGAAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCCTACAAA 1030         :::
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|ProAlaThrAlaLysArgGlyArgSerArg---SerArgThrProThrLysArgGlyHis 505
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ProThrLysValSerArgHisAlaSerSerProGluSerProLysProAlaProAla
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APPLICANT: Lorens, James B.
APPLICANT: Atchison, Robert E.
APPLICANT: Atchison, Robert E.
APPLICANT: Atchison, Robert E.
APPLICANT: Holland, Sacha
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APPLICANT: Holland, Sacha
TILE REPERENCE: 021044-005820US
CURRENT APPLICATION NUMBER: US,10/696,909A
CURRENT APPLICATION NUMBER: US 60/512,251
PRIOR APPLICATION NUMBER: US 60/421,989
PRIOR FILING DATE: 2003-10-17
PRIOR FILING DATE: 2003-10-29
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 44
LENGTH: 2752
                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: splicing coactivator subunit SRm300; RNA binding OTHER INFORMATION: protein; AT-rich element binding factor
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22 SerSerSerSerSerValProlleProSerThrThrSerValGlnProSerSerSer 41	216ACCTGCTCGACGACCCCCACGAAGCCCTTGCCGCGCGCGC	42 GlySerAlaProThrThrSerAlaThrSerValGlnThrSerSerSerSerProPro 61	261 TTATCGAATCTGCCGAACACAGCCTCGATTTGCAATACTTTGGCGCAACGACATTT 320 :::	321 CCGGCAGGCTGCTGTTCAACCTCATGTACCTTGCCGCGAACGCGGCGTGCGCGTACGCC 380	TGCTGTTGGACGACAACAACGCGCGCTTGGACGATCTCCTGCTCGCCCTCGACGACGACCC	93FROINTINIARGALAINISSELVAIGINSEISEISEISEISEISEI 10/ 441 ATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCTACGCAAATGGCGCGCACTCG 500		501 GCTACCTGACCGACCGCCCGCCTCAACCGCCGCATACAACAAATCCTTTACCGCCG 560	561 ACAACC		588 GCAATATCGGCGAATACTTCAAAGTCGGTGAGGACACCGTTTTCG 635	162 ValSerValGlnProSerSerSerSerSranaProThrThrSerAlaThrSerValGln 181	636 CCGACCTGGACTCCTCGCCACCGGCGACGTCGCCGAAGTATCGCACGACTTCG 692	182 ProSerSerSerSerSerProProlleSerSerThrValSerValGlnThrSerSerSer 201	693ACGGCTACTGGGCAAGCCATTCGGCCACAAGGCACGCGCATCA 737	202 SerSerValProThrThrSerThrThrSerValGlnProSerSerSerSerValPro 221	738 TCCGCAGCGCAACATCGCAAGGTCTTCAAGCACTCGGATACA 782	ThrThrSerAlaThrSerValArgSerSerSerSerSerThrProlleProSerThr	/83 ACGACGARALCAGAC	CGGTCGAACAGTCGCCCCTCTACCAAAAATACAGACGGGACGCATCG		873 ACTGGCAGAGCCTCCAAACCCGCCTGATCAGCGACACCCCTGCAAAAGGACTCGACCGCG 932		933 ACCGCCGCAAACCGCCGATTGCCGGGAGGCTGCAAGACGCCGCTCAAACAGCCCGAAAAAA 992	298SerSerProProlleSer 303	993 GCGTCTATCTGGTTTCACCCTATTTCGTCCCTACAAAATCCGGCACAGACGCACTGGCAA 1052	304 SerThrileSerValGlnProSerSerSerSerSerProThrThrSer 320	AACTGGTGCAGGACGGCATAGACGTTACCGTCCTGACCAACTCGCTACAGGCGACGACG		1113 TTGCCGCCGTCCATTCCGGCTACGTCAAATACC
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267 AATCTGCCGAACACACCTCGATTTGC	CGCGCGGTTGGACGATCTCCTGCTCGCCTT     ::     ::     ::     ::	456			1086 TGACCAACTCGCTACAGGCGACCGACGTTGCCGCCATCCATTCCGGCTACGTCA 1139 
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Qy         1146	1293TCGGCTCATTCAACCTCGACCCCCGTTCCGCA 	TIGHT	Qy         1437 AACACAACCGCCTGCAATGGCACGATCCCGCCACCGAAAAACCTACCCGAACG 1490           Db         464 SerAlaThrSerValGlnProSerSerSerSerSerProProIleSerSerThrIle 482           Qy         1491 AACCCGAAGCCAAACTTGGAAACGCATCGCCGCAAAAATCC 1532           C         11491 AACCCGAAGCTTGGAAACGCATCGCCGCAAAAATCC 1532	RESULT 21 US-10-437-963-125004 US-10-437-963-125004 Sequence 125004, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J. APPLICANT: APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Bunkharov, Andrey A. APPLICANT: Bunkharov, Andrey A. APPLICANT: Bunkharov, Andrey A. APPLICANT: Bunkharov, Andrey A. APPLICANT: Bunkharov, Andrey A. APPLICANT: Bunkharov, Andrey A. APPLICANT: Bunkharov, Blants and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: 10-213 CURRENT APLICATION NUMBER: US/10/437,963 CURRENT FILE DEFENCE: 38-21 (5322)B CURRENT FILE OF INVENTION NUMBER: US/10/437,963 CURRENT APLICATION NUMBER: US/10/437,963 CURRENT APLICATION NUMBER: US/10/437,963 CURRENT APLICATION NUMBER: US/10/437,963 CURRENT APLICATION UNBURE at all Xa locations FEATURE: NUMBER OF SEQ 10 NOS: 204966 I.OCATION: (1): (497) COTHER INFORMATION: Clone ID: PAT_MRT4530_27690C.1.pep Alignment Scores: COTHER INFORMATION: Clone ID: PAT_MRT4530_27690C.1.pep Bercent Similarity: 27.2* Rescret Local Similarity: 27.2* Rescret Local Similarity: 27.2* Rescret Local Similarity: 27.2* Rescret Local Similarity: 27.2* Rescret Local Similarity: 27.2*	DIMITIALITY: 27.28 INDELS: 10.4% Indels: 4 Gaps: 990A-13 (1-1561) x US-10-437-963-125004 (1-4

Qy         100 GCCCCCACTGGAAGAACGGACGGAAAGCCGTCATTCAATACTTCCAAACCTGTCCTCT 159	Db 18283 ArgArgGlyProLeuCysProGlyAsnSerAlaSerProProProCysGlyArg 18300  Qy 306 GGGCAACGACATTTCCGGCAGGCTGCTGTTCAACCTCATGTACCTTGCCGCAG 359	455 1835 515 1836 572	CCATACTCGGCGGACGAATATCGGCGACGAACGATCTTCAAAGTCG :::   :::   :::	708 GCCATTCGGCCAAGGCACGGGATCATCGGCAGGGGAACATCGGCAAGGGTC 18450 ProGluProProThrThrProThrLysAlaAlaAlaValCysSerTrpSerAlaArg 765 TTCAAGCACTCGGATACAAGGAAACATCCAGACACGCGCTCCTGCGCTACGGGAAA 18469TrpProThrSerGlyAlaTspalaSerGluArg 825 CGGTCGAACACGCCCTCTACCAAAAAATACAGA	
Qy         1140 AATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCATG 1199           Db         328 ProAlaThrGlyThrProProSerProThrThrSerSerProThrAla 345           Qy         1200 CCGTCCCGGCA	1344 GCGTCGTCATCGAAAGCCCCAAAATCGCAGAACAGATGGAGCGCACCCTCGCCGATA	Db 424 ThrSerSerThrCysProProAlalleThrSerArgProThrSerProAlaCysHis 443  Qy 1485	VS-10-084-846A-5  i Sequence 5, Application US/10084846A  j Publication No. US20040006026A1  j GENERAL INPORMATION:  APPLICANT: WEITNAUER, GABRIELE  j APPLICANT: WHILENWEG, AGNES  j APPLICANT: BECHTHOLD, ANDREAS  j TILE OF INVENTION: AVILAMYCIN DERIVATIVES  j FILE REFERENCE: 1974-005  CURRENT APPLICATION NUMBER: US/10/084,846A	; CURRENT FILING DATE: 2003-02-25 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815 ; PRIOR FILING DATE: 2001-08-24 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4 ; PRIOR FILING DATE: 2001-02-25 ; NUMBER OF SEQ ID NOS: 120 ; SEQ ID NO 5 ; LENGTH: 19723 ; TYPE: PRI	JOURNAL STITE PROGRAMMY STATE OF STATE

; ORGANISM: Xanthomonas ; FRATURE: US-10-418-861B-59 Alignment Scores: Pred: No.: Score: Score: Score: Percent Similarity: Best Local Similarity: 10.4\$ Gaps:  Indels: 14  Indels: 16  Indels: 16  Indels: 16  Indels: 16  Indels: Ind	US-10-665-990A-13 (1-1561) x US-10-418-861B-59 (1-486) Qy 83 TCATGTTCATGGTTGCCCCACTGGAAGAACGGAAAGCCGTCATTCAATACT 142	Db 89 HI	103	118 ATAINICIUVAIHISIIDDBUVAIASPGIYAIAALAINIIJITALAAAAILELIBGIUALA 263 ATCGAATCTGCCGAACAGCCTCGATTTGCAATACTACATTTGGCGCAACGACATTTCC 	Db 138 ileArgGlyAlaArgAspHisIleHisLeuGluTyrTyrIlePheGlnProAspHisSer 157  Qy 323 GGCAGGCTGCTGTTCAACCTCATGTACCTTGCCGCGGAGAACGCGGCGTGCGCGTACGCTG 382	Db 158 dlynkalailecysalaalaieuMetGluargalaargaladlyvaliysValakgleu 177  Qy 383 CTGTTGGACGACAACACGCGGGGGTTGGACGATCTCCTGCTGGCCTCGACGACCAT 442	MalalleGlySerSerAlam GGAGTGCGCCTGTTCAACC	Db 198 AlaGlyValGluThrAlaTrpPheHisFroSerGlnLeu	Db 211LeuLysProPheLysArgProTrpLeuAsnLeuArgThrHisArgLysValIleVal 229  Qy S57 GCCGACACCCACCATACTCGGCGACGCAATATCGGCGACGAATACTTCAAAGTC 616	Db 230 IleAspGlyArgIleGlyPheThrGlyGlyIleAsnValThrAspAspGluAsnGluGln 249 Qy 617 GGTGAGGACACCGTTTTCGCCGACCTGGACATCGTCGCCACGGCAGCGTCGTCGTCGAA 676	250	Qy 677 GTATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAACGCCATC 736	Oy 737 ATCCGCAGCAACATCGCCAAGGGTCTTCAAGCACTCGGATACAACGAAGAACTCC 796	Qy 797 AGACACGCCTCCTGCGCTAACACGTCGAACAGTCGCCCTCTACCAAAAATA 856	857 CAGACGGGACGCATCGCAGAGCGTCCAAACCCGCCTGATCAGCGACACCCCTGCA	Db 314 SerGlyProAspSerSerTrpGluAlaIleHisArgLeuMetValAla329	Qy 917 AAAGGACTCGACCGCGCAAACCGCCGATTGCCGGGAGGCTGCAAGACGCGCT 976       ::
Qy         928	Qy 1080 CCGTCCTGACCAACTCGCTACAGGCGACCGATGCCGCCGTCCATTCCGGCTACGTCA 1139  Db 18617ProThrAlaThrArgSerArgProProArgArgArgProArgAr 18631	OY 1140 AATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAAC 1190 i	1191TCCCCG   1191	Qy 1209 CCACAAAAAACACAAGGCCGGGAAGCTCGGAAACCGTCATCA 1268 	Qy 1269 TTGTGGACGCAAACGCATCTTCATCGGCTCATTCAACCTCGACCGCTTCCGCACGGC 1328	Oy 1329 TCAATACCGAAATGGGCGTCGTCATCGAAAGCCCCAAAATCGCAGAACAGATGGAGGGCA 1388 1::     :::     Db 18707 ThrThrProSerThrThrProProArgThrAlaThrAlaArg 18724	Oy 1389 CCCTCGCCGATACCACCCGAATACGCCTACCGCGTTACCCTCGACAAACACCGCC 1448	OY 1449 TGCAATGGCACGATCCGCCACCCGAAAACCTACCCGAACCGAAGCCAAACTTT 1508  Db 18745 SerAlaCysThrThrProAlaArgAlaProProProArgSerSerProAlaSerThrGly 18764	Qy 1509 GGAAACGCATCGCCGCAAAAATCCTGCTGCCCATCG 1550  1509 GGAAACGCATCGCCGCAAAAATCCTGCTGCCCATCG 1550  18765 SerProGlyThrProSerSerArgProSerProThrCysProSer 18779	RESULT 23 US-10-418-861B-59 ; Sequence 59, Application US/10418861B	n No. US20040010131A1 FORMATION:		APPLICANT: Ferro, Jesus Aparecido APPLICANT: De Oliveiro, Julio Cezar Franco APPLICANT: De Laia, Marcelo Luiz APPLICANT: Setubal Joao C.		CURRENT APPLICATION NUMBER: US/10/418,861B; CURRENT FILING DATE: 2003-04-17	; PRIOR APPLICATION NUMBER: US 60/374,620 ; PRIOR FILING DATE: 2002-04-22 . NITMERD OF SEC ID MCS. RE	; SEQ ID NO 59 ; EBNCTH: 486 ; TYPE: PRT

126 GCCGTCATTTCAATACTTCCAAACCTGTCCTGGACAACATCCTGCAAATCCGGCACA    :::           :::	y 186 CCCCTCATAACAACGGGCTATCCGACATCTACCTGGTCGACGACCCCCAGAAGCCCTTG 245	y 246 CCGCCGCCCCTTATCGAATCTGCCGAACACAGGCTCGATTTGCAATACTACATTT 305	306 GGCGCAACGACATTCCGGCAGGCTGCTGTCAACCTCATGTACCTTGCCGCAGAACGCG	y 366 GCGTGCGCGTACGCCTGCTGGACGACAACAACACGCGCGGGGTTGGACGATCTCCTGC 425	y 426 TGGCCCTGGACAGCCATCCCAATATGGAAGTGGGCCTGTTCAACCCCTTGGTCTACGCA 485	y 486 AATGGCGCACTCGGCTACCTGACCGACTTCCCCGGCCTCAACCGCCGCATGC 539	y 540 ACAACAAATCCTTTACCGCCGACAACCGCGCCACCATACTCGGCGACGCAATATCGGCG 599	y 600 ACGAATACTTCAAAGTCGGTGAGACACCGTTTTCGCCGACCTGGACATCCTCGCCACG 659	y 660 GCAGCGTCGTCGCGAAGTATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCC 719	y 720 ACAACGCCACGCATCATCCGCAGCGCAACATCGGCAAGGGTCTTCAAGCACTCGGAT 779	780	y 840 CCCTCTACCAAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCC 896	897	957	1017	1077 TTACCGTCCTGACCAACTCGCTACAGGCGACGTTGCCGCCGTCCATTCCGGCTACG	1137 TCAAATACCGAAAACGCTGCTCAAAGCCGCGTTCAAACTTTACGAGTGCAACCCAACC	323
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977 AAACAGCCCGAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCCTACAAATCCGGC ::: ::: :::	<pre>uy</pre>	Oy 1097 CTACAGGCGACCTTGCCGCCGTCCATTCCGGCTACGTCAAATACCGAAAACGCTG 1156	Qy     1157 CTCAAAGCCGGGATCAAACTCTAGGAGCTGGAACCCAACCATGCCGTCCCCGCCACAAAA 1216	OY 1217 GACAAAGGCCTGACCGGCAGCTCCGTAACCAGCTGCATGCCAAAACCTTCATTGTGGAC 1276	OY 1277 GGCAAACGCATCTTCATCGGCTCATTCAACCTCGACCCCCGTTCCGCACGGCTCAATACC 1336  Db 413 AspaspValCysIleValGlySerAlaAsnPheAspSerArgSerPheArgLeuAsnPhe 432	Oy 1337 GAAATGGCCGTCCTCATCGAAAGCCCCAAAATCGCAGAACGAGGGGCGCCCCTCGCC 1396	OY 1397 GATACCACCGGAATACGCCTACCGCGTTACCCTCGACAAACACACAC	Qy 1457 CACGATCCGCCACCGGAAAACCTACCGGAACCGAAACCGAAACTTTGGAAACGC 1516	Oy 1517 ATCGCCGCAAAAATCCTATCCTGCTG 1543  Db 478PheAlaArgLeuLeuSerProLeu 485	RESULT 24 US-10-626-832-86 S. Sequence 86, Application US/10626832	PUBLICATION NO. USZUUSOU01342A1 GENERAL INFORMATION: APPLICANT: Davis Poynter, Nick APPLICANT: Nugert, Josephine	APPLICANT: BICH-MACHIN, 1AN APPLICANT: BICH-MACHIN, 1AN TITLE OF INVENTION: Viral Marker FILE REFERENCE: 620-262	CURRENT APPLICATION NUMBER: US/10/626,832 CURRENT FILING DATE: 2003-07-25 PRIOR APPLICATION NUMBER: US 60/398,576 PRIOR FILING DATE: 2002-07-26	NUMBER OF SEQ ID NOS: 259 SOFTWARE: PatentIn version 3.1 SEQ ID NO 86 LENGTH: 866	; TYPE: PRT ; ORGANISM: Equine herpesvirus 1 US-10-626-832-86	3.45e-11 Length: 293.50 Matches:	Best Local Similarity: 25.1% Mismatches: 220 Query Match: 10.3% Indels: 85 Gaps: 13	

1197 ATGCCGCCACAAAAGACAAAAGGCCTGACCGCAACCAGCCTGCTG 1256  343 SerThrSerThrProSerAlaSerThrAlaThrSerAlaThrPro	8 8 8 8 8 8 8 8 8 8	1 4 9 3 7 2 9 9 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
ThrThrSerAlaThrThrThrAlaPheThrThrGluSerHisThrSerProAspSerSer 436  TTTGGAAACGCATCGCCGCAAAAATCCTATCCT	8 8 8 8	109 gAlaProSerThrValProAlaValSerSerGlySerAlaAlaSerSerSerThrSe 129 437 AGCCATCCCAATATCGAAGTGCGCCTGTTCAACC
Sequence 174113, Application US/10437963  Sequence 174113, Application US/10437963  GENERAL INFORMATION:  APPLICANT: La Rosa, Thomas J.  APPLICANT: Kovalic, David K.  APPLICANT: Tanua  APPLICANT: Wu, Wei  APPLICANT: Wu, Wei  APPLICANT: Buckharov, Andrey A.  APPLICANT: Li, Ping  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  FILLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  FILLE OF INVENTION: Rice Nucleic Acid Molecules Associated With  FILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  FILLE DATE: 2003-05-14  NUMBER: US/10/437,963	8 8 8 8 8 8 8 8	
WMBEN OF SEQ ID NOS: 204966  Q ID NO 174113  LENGTH: 465  TYPE: PRT  ORGANISM: Oryza sativa  NAME/KEY: unsure  LOCATION: (1)(465)  OTHER INFORMATION: unsure at all Xaa locations  OTHER INFORMATION: Clone ID: PAT_MRT4530_72086C.1.pep	8 8 8 8 8 8	
Alignment Scores:  Pred. No.: 293.00 Matches: 148 Score: Score: Similarity: 26.9\$ Mismatches: 172 Guery Match: 4.0.3\$ Mismatches: 161 Gaps: 18-10-665-990A-13 (1-1561) x US-10-437-963-174113 (1-465)  Qy RGTTCATGTTCATGTTGTTCATGGTTGCCCCACTGGAAGACGGGAAGCCGTCATTTCAAT 139 A CysSerCysSerSerSerSerSerSerSerSerSerAlaAlaSerPro 23	8 6 6 6 6 6 6	ATTGCCGGGAGCTGCAAAC

US-10-665-990A-13 (1-1561) x US-10-437-963-176617 (1-533)	Qy 154 CCTCCTGGACAACATCCTGCAAATCCGGCACCCCTCATAACAACGGGCTATCCGACAT 213	Qy 214 CTACCTGCTCGACGACGCCCTTGCCGCGCGCGCCGCCCTTATCGAATCTGC 273	Qy 274 CGAACACGGCTCGATTTGCAATACTACATTTGGCGCAACGACATTTCCGGCAGGCTGCT 333	Qy 334 GTTCAACCTCATGTACCTTGCCGCAGAACGCGGCGTGCGCGTACGCCT 381	Oy 382 GCTGTIGGACGACAACACGCGCGGGGTTGGACGATCTCCTGCTCGCCTCGACAGCCA 441	Qy 442 TCCCAATATCGAAGTGCGCTGTTCAACCCCTTCGTCCTACGCAAATGGCGCGCACT 498	Qy 499 CGGCTACCTGACCGCCTCAACCGCCGCATGCACAAAT 548	Qy 549 CCTTTACCGCCGACAACCGCGCCACCATACTCGGCGACGCAATATCG 596	Qy 597 GCGACGAATACTICAAAGICGGTGAGGACACCGTTITCGCCGACC 641 :::	Qy 642 TGGACATCCTCGCCACCGCAGCGTCGTCGACGCAAGTATCGCACGACTTCGACCGCT 698	QY 699 ACTGGGCAAGCCATTCCGCCACAAGGCGACGCGCATCATCCGCAGGGCAACATCGGCA 758 :::	QY 759 AGGGTCTTCAAGCACTCGGATACAACGACGAAACATCCAGACACGCGCTCCTGCGCTACC 818	QY 819 GCGADACCGTCGAACAGTCGCCCTCTACCAAAAATACAGACGGGACGCATCGACTGGC 878	QY 879 AGAGGTCCAAACCGGCTGATCAGGGACACCCCTGCAAAAGGACTCGACCGCGACCGC 938	QY         939         GCAAACGCCGATTGCCGGGAGGCTGCAAGACGCGCTCAAACACGCGCTCAAAAAAAGCGTCT         998           Db         227	999 ATCTGGTTTCACCCTATTTCGTCCCTACAAAATCCGGCACAGACGCACTGGCAAAACTGG	UD 230FIOATODEURTOPIOPTORIOPIOASPATOAIASSETUTRATGSSETCIYASB1 245 QY 1059 TGCAGGACGATAGACGTTACCGTCCTGACCAACTCGCTACAGGCGACCGAC	Db 246ValAspProCysPro 250	Qy 1119 CCGTCCATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCT 1178
	OY 1127 TCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGCATCAAAACTCTACGAGCTG 1186 1:	OY 1187 CAACCCAACCATGCCGCCACAAAAGACAAAAGGCCTGACGGCAGCTCCGTAACC 1246	Qy 1247 AGCTGCATGCCAAAACTTCATTGTGGACGGCAACGCATCTTCATCGGCTCATTCAAC 1306	Qy 1307 CTCGACCCCGTTCCGCACGGCTCAATACCGAAATGGGCGTCGTCATCGAAAGCCCCAAA 1366	OY 1367 ATCGCAGAACAGGCACCCTCGCCGATACCACACCCGAATACGCT 1418	Qy 1419ACCGCGTTACCCTCGACAACACAACGCCTGCAATGGCAC 1459  Db 408 rSerSerAlaArgArgArgArgSerProSerProThrArgArgTrpThrSerCysSerGlyTh 428	Qy 1460 GATCCCCCCCCCCACCCGAAAACCTACCCGAACCAAACCCAAACTTTGGAAACGC 1516	Qy 1517 ATCGCCGCAAAATCCTATCCTGCTGC 1544	RESULT 26 US-10-437-963-176617 Sequence 176617, Application US/10437963 Publication No He200401323231	GENERAL INFORMATION: ; APPLICANT: La Rosa, Thomas J. ; APPLICANT: Kovalic, David K. sabb:roant: 75001		222	; FILE KEFEKENCE: 38-21(93221)B ; CURRENT APPLICATION NUMBER: US/10/437,963 ; CURRENT FILING DATE: 2003-05-14 ; NUMBER OF SEQ ID NOS: 204966	; SEQ 1D NO 1/051/ LENGTH: 533 ; TYPE: PRT ; ORGANISM: Oryza sativa	<pre>// FEALUKE: // NAME/EX: // LOCATION: (1)(533) // OTHER INFORMATION: unsure at all Xaa locations</pre>	; FEATURE: ; OTHER INFORMATION: Clone ID: PAT_MRT4530_74349C.1.pep US-10-437-963-176617	Length:	t Similarity: 34.3% ocal Similarity: 26.8%	10.3% Indels:

122 TyrAsnAsnAlaAlaPheLeuThrThrAspAsnAspLeuThrIleTyrThrAspGlyHis 141	236 GAAGCCCTTGCCGCCCGCCCCTTATCGAATCTGCCGAACACAGCCTCGATTTGCAA 295 .::	296 TACTACATTIGGGGAAGGACATTICCGGCAGGCTGCTGTTCAACCTCATGTACCTTGCC 355	356 GCAGAACGCGGCGTGCGCTGCTGTTGGACGACAACAACAACGGGGGGTTGGAC 415	416 GATCTCCTGCTCGCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCCTTC 475	476 GTCCTACGCAAATGGCGCGCACTCGGCTACCTGACCGACTTCC	521	566 CGCGCCACCATACTCGGCGACGCAATATCGGCGAAGAATACTTCAAAGTCGGTGAGGAC 625 ::	626	677 GTATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAACGCCACGCGC 733 :::	734	773	833	890ACCGGCTGATCAGCGACACCCCTGCAAAAGGACTCGACCGCGACAAA 334 GlytyrLeuLysMetllSerSerAla	944	1004	1064 GACGCATAGACGTTACCGTCCTGACCAACTCGCTACAGGCGACCGAC	1124 CATTCCGGCTACGTCAAATACCGAAAACCGCTCAAAGCCGGCATCAAACTCTACGAG 1183	1184
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LysMetAlaAsnPheAspHisPhe	341
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RESULT 30
US-10-429-094-18
US-10-429-094-18
Sequence 18, Application US/10429094
Publication No. US20030180821A1
GENERAL INFORMATION:
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                                                                                                                       Sequence 18, Application US/09966521

Publication No. US20030087321A1
GENERAL INFORMATION:
APPLICANT: TOUINN, Cheryl
APPLICANT: ARVIDSON, Staffan
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Conservative:
Mismatches:
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286.50
38.2%
21.1%
                  CTATCC 1537
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Best Local Similarity:
Query Match:
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LysGluSerTyrAlaAsnArgProLeuSerValLysPheLysGluSerLeuAlaLysLeu 488
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274 AspAlaValAspAlaLeuGlnLeuArgPheIleLeuAspTrpAsnSer---GlnAlaHis
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328 GlnIleGluTyrGlyTyrThrLysMetIleMetSerAla--------
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254 GluTyrLeuGlyLveuGlyLysLeuGlyTyrTrpArgAspThrHisLeudRrgIleGlnGly
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GAATACTTCAAAGTCGGTGAGGACACCGTTTTCGCCGACCTGGACATCCTCGCCACCGGC
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1112 GTTGCCGCCGTCCATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCATC 1171
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381 HisProLeuValTyrTrpAlaThrPheSerAsnAlaSerAspLeuLeuSerSerGlyVal 400
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328 GlnIleGluTyrGlyTyrThrLysMetIleMetSerAla---------
       --CGCAGCGCCAACATCGGCAAG
                                                                    GGTCTTCAAGCACTCGGATACAACGACGAAACATCCAGACACGCGCTCCTGCGCTACCGC
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; Sequence 90, Application US/09828523A
; Patent No. US20020168697A1
; GENERAL INFORMATION:
    APPLICANT: The Pharmacia & Upjohn Company
    TITLE OF INVENTION:
    TILE OF INVENTION: 268.63120101
; CURRENT APPLICATION NUMBER: US/09/828,523A
; CURRENT FILING DATE: 2001-04-06
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 99
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444 ValTyrAspGluAsnLeuAlaLysAspLeu-------
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            APPLICANT: QUINN, Cheryl
APPLICANT: ARVIDSON, Staffan
APPLICANT: HARIS, Douglas
APPLICANT: HARIS, Douglas
APPLICANT: HARIS, Douglas
FILE REFERENCE: 00774 USL CN1
FILE REFERENCE: 00774 USL CN1
CURRENT APPLICATION NUMBER: US 010429, 094
CURRENT FILING DATE: 2003-05-02
PRIOR PILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 145
SOFTWARE: PATENTIN VETSION 3.0
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Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Staphylococcus aureus
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38.2%
21.1%
10.0%
TOMICH, Che-Shen
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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US-10-429-094-18
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TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Amino acid sequence encoded by S. aureus coding region cloned for
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GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT TOMICH, Che-Shen
APPLICANT: QUINN, Cheryl
APPLICANT: ARVIDSON, Staffan
APPLICANT: HARIS, Douglas
APPLICANT: HARIS, Douglas
APPLICANT: HARIS, Douglas
TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
FILE REFERENCE: 6212 NZ
CURRENT APPLICATION NUMBER: US/09/966,521
CURRENT APPLICATION NUMBER: 2001-09-28
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentin version 3.0
SEQ ID NO 84
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Matches:
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                                 LENGTH: 502
TYPE: PRT
ORGANISM: Artificial Sequence
 SOFTWARE: PatentIn version 3.1
SEQ ID NO 90
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286.50
38.2%
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Best Local Similarity:
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US-09-828-523A-90
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382 HisProLeuValTyrTrpAlaThrPheSerAsnAlaSerAspLeuLeuSerSerGlyVal
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Publication No. US20030180821A1

GENERAL INFORMATION:
APPLICANT: TOMICH, Che-Shen
APPLICANT: TOMICH, Che-Yl
APPLICANT: ARVIDSON, Staffan
APPLICANT: HARRES, Douglas
APPLICANT: MOTT, John
ITILE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
FILE REFERENCE: 00774, US1 CN1
CURRENT APPLICATION NUMBER: US 09/966,521
PRIOR APPLICATION NUMBER: US 09/966,521
PRIOR PLILING DATE: 2001-09-28
SOFTWARE: Patentin version 3.0
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ORGANISM: Artificial
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LysMetAlaAsnPheAspHisPhe------LysSerLeuGlyGlyGluVal
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EXPRESSION OF 10,000 OR
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Matches:
Conservative:
Mismatches:
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                                                           SQUENCE 41094, Application US/11097143
Publication No. US2005020858A1
GENERAL INFORMATION
TITLE OF INVENTION: DETECTION KIT, SUCH AS MI TITLE OF INVENTION: DETECTION KIT, SUCH AS MI TITLE OF INVENTION: DETECTION KIT, SUCH AS MI TITLE OF INVENTION: DECONORA
FILE REFERENCE: CLOGO728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
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PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 2000-01-2
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-2
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEC ID NOS: 43008
SOFTWARE: FESSEE FOR WINGOWS VERSION 4.00
SEC ID NO 41094
LENGTH: 2284
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us-10-665-990a-13.rapbm

Oy 276 AACACAGCCTCGAITTGCCAATACTACATTTGCGCGCAACG	315	Qy         375 TACGCCTGCTGTTGGACGACGACAACAACAACAACAACAACGGGGGGTTTGGACGATCTCCTGC	Qy 426 TCGCCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCTACGCA :::	486	Qy 546 AAICCITTACGGCGACAACGGGGCACCATACTGGGGAATATGGGGGAAGAAT	Qy 606 ACTICAAAGICGGTGAGGACACCGITITGGCCGACCIGGACAICCTCGCCACCG :::::: ::	Qy 660 GCAGCGTCGTCGGCGAAGTATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCC	With Db ThrargSerArgArgAlaSerAlaAlaSerProProSerFroSerThrargArgSerArgArgArgArgArgArgSerAlaAlaSerAlaAlaSerProProSerFroSerThrargArgSer	Qy 780 ACAACGACGAAACATCCAGACACGCGCTCCTGCGCTACC	Qy 819 GCGAAACGGTCGAGTGGCCCCTCTACCAAAAATACAGACGGGACGCATCGACTGGC	Qy 879AGAGGTCCAAACCGCCTGATCAGCGACCCCTGCAAAAGGACTCGACCGCG ::	Qy 933 ACCGCCGAAACCGCCGATTGCCGGGAGGCTGCAAGACGCGCTCAAACAGCCCCGAAAAAA	202 993 272 1053	292		Qy 1173 AACTCTACGAGCTGCAACCCATGCCGTCCCGGCACAAAAGACAAAGGCCTGACCG	Qy 1233 GCAGCTCCGTAACCAGCCTGCAAAACCTTCATTGTGGACGCAAACGCATCTTCA
OY 1294 CGGCTCATTCAACCTCGACCCCGTTCCGCACGCTCAATACCGAAATGGGCGTCGTCAT 1353  Db 557 ArgSerProSerProAlaProPro	GATGGAGCGCACCCTCGCCGATACCACCCGAATA	Qy 1414 CGCCTACCGCGTTACCCTCGACAAACACCGCTGCAATGGCACGATCC 1464 	QY 1465 CGCCACCGAAAAACCTACCCGAACGCGAAGCCAAACTTTGGAAACGCATCGCCGC 1524	Qy 1525 AAAAATCCTATCCTGCTGCCCATCGAAGG 1554	RESULT 37 US-10-437-963-199493 Sequence 199493 Application US/10437963 Publication No. HS2004012334331	GENERAL INFORMATION: ; APPLICANT: La Rosa, Thomas J. ; APPLICANT: Kovalic, David K.	Znou, Xinu Cao, Yongw Wu, Wei Boukharov,	; APPLICANT: Barbazuk, Brad ; APPLICANT: Li, Ping ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement	; FILE REFERENCE: 38-21(53221)B ; CURRENT APPLICATION WNDER: US/10/437,963 ; CURRENT FILING DATE: 2003-05-14 ; NUMBER OF SEQ ID NOS: 204966	; SEQ ID NO 199493 ; LENGTH: 427 ; TYPE: PRT ; ORGANISM: Oryza sativa	<pre>; FEATURE:</pre>	; FEATURE: ; OTHER INFORMATION: Clone ID: PAT_MRT4530_95052C.1.pep US-10-437-963-199493	ignment Scores: 2.88e-10 2re: 279.00 rcent Similarity: 81 Local Similarity: 25.08 ery Match:	Gaps: ) x US-10-437-963-199493 (1-4	Qy 105 CACTGGAAGAACGGACAGAAAGCCGTCATTTCAATACTTCCAAACCTGTCCTCTGGACA 164 :::               :::  bb 6 TyrTrplysValGlyLVsThrMetThrArdLysAsD 17	ACATCCTGCAAATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACC	219TGCTCGACCACCACAAGCCCTTGCCGCCCGGGG

359 Db 119 ProSerThr	CCCGGAAT 1412	1472 Qy 384 399 Db 145	Oy 444 CCAATATCGAAGTGCGCCTGTTCA	Qy 468 ACCCCTTCGTCCTACGCAAATGGCGGCACTCGGCTACCTGACCGACTTCCCCCGCCTCA	Qy 528 ACCGCCGCATGCAACAAATCCTTTACCGCCGACAACCGCGGGGGGGGGG	Qy         570 CCA	www.molecules Associated With bb 243 ProSerSerGlySerSerProThrThrProGlyGlyGlyGlyGlyGlyGlyGlyThrProThrPro	CURRENT APPLICATION NUMBER: US/10/437,963  CURRENT FILING DATE: 2003-05-14  Db 263 SerAspThrProSerSerAgThrThrProGlyGlyGsysSer	Oy 705 Db 283	Qy         765 TTCAAGCACTCGGATACAACGACGAAACATCCAGACACCGCTCCTGCGCT	Qy 816 ACGCGGAAACCGTCGAACAGTCGCCCCTCTACCAAAAATACAGACGGACG	Qy 876 GGCAGAGCGTCCAAACCCGCCTGATCAGCGACCCCTGCAAAAGACTCGACCGCGGACCGCACC	Oy 936 GCGGCAAACGGCGGATGGCGGGAGGCTGCAAGACGCGCTCA ::: Db 347 GlyThrSerProthrThrProGlyGlyGly	TCTCTGTTCAGGTTTCACCCTATTTCGTCCTACAAAAACGGCACAGGTAAAATCCGGCACAG  TTCTCTGTTCATGTTCATGGTTGCCCCCACTGGAAAAAAGGGACGACATT 134  TCTCTGTTCATGTTCATGGTTGCCCCCACTGGAAAAAAGGGACGATT 134  TCTCTGTTCATGTTCATGGTTTCGTCCTACAAAAAAAAAA	CTCATA	AGGCGACGTTGCCGCCGTCCACGAGGCTACCGACGTTGCCG
	353 TCGAAAGCCCCAAAATCGCAGAACAGATGGAGCGCACCCTCGCCGATACCACACGGATA	ACGCCTACCGCGTTACCCTCGACAAACACGCCTGCAATGCGATCCGCCACCC					Othe nt 1			OTHER INFORMATION: Clone ID: PAT_MRT4530_36471C.1.pep 0-437-963-134726	668 145 57	21.0	-668) C :	GGACO	TCCGG	CCCA

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Db 433 GlyGlyAsnTyrProProAlaProThrIleGlyAsnValProProSerForSerSerGly 452  Qy 1224 GCCTGACCGCAGCTCCGTAACCAGCTGCATGCCAAACCTTCATTGTGGACGCAAAC 1283  Db 453 ThrSerProSerThrProGlyGlyClyCysSerSerSerProThrProCysAspAlaPro 472  Qy 1284 GCATCTTCATCGGCTCATTCAACCTCGCACGGCTCA	RESULT 39 US-10-084-846A-8 US-10-084-846A-8 US-10-084-846A-8 Sequence 6, Application US/10084846A FUDLICATION NO. US20040006026A1 GENERAL INFORMATION: APPLICAMY: WHITMAUER, GARRIELE APPLICAMY: BECHTALD, ANDREAS TITLE OF INVENTION: AVILAMYCIN DERIVATIVES FILE REFERENCE: 1974-005 CURRENT APPLICATION NUMBER: US/10/084,846A CURRENT APPLICATION NUMBER: PCT/EP01/09815 FRIOR APPLICATION NUMBER: DE 101 09 166.4 FRIOR APPLICATION NUMBER: DE 101 09 166.4 FRIOR APPLICATION NUMBER: DE 101 09 166.4 FRIOR APPLICATION NUMBER: DE 102-02-25 NUMBER OF SEQ ID NOS: 120 SOFTWARE: PATENTIN Ver. 3.2 SOFTWARE: PATENTIN Ver. 3.2 SEQ ID NO 8 LENGTH: 19608 TYPE: PRT ORGANISM: Streptomyces viridochromogenes FEATURE: OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1. COTHER INFORMATION: Start codon: atc, Start position: nucleotide 3. US-10-084-846A-8	Alignment Scores:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 IleHisGluLysAsnSerProAspThrSerPhePheLeuArgLeuIleLysGluTrpSer 198
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6 Prollebys1leAlaPheGluLysAlaLeuLysAsnAlaLysGluSerValPheIleAla 25
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                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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US-10-335-977-9083
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Best Local Similarity:
Query Match:
DB:
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Job time : 426 secs
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5455 oCysSerProArgThrArgThrSerArgArgArgArgProGlyArgSerThrSerArgSe 5475
                                         ACCGGCAGCTCCGTAACCAGCCTGCATGCCAAAACCTTCATTGTGGACGGCAAACGCATC 1288
                                                                                                                                                                5515
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                                                                                                                   1289 TTCATCGGCTCATTCAACCTCGACCCCCGTTCGGCGCTCAATACCGAAATGGGCGTC
                                                                                                                                          5531 pProThrSerThrThrProSerProAlaArgThrArgThrAlaProSerArgArgThrPr
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                                                                                                                                                                                                                                                                           1406 CCCGAATACGCCTACCGCGTTACCCTCGACAACACAACCGCCTGCAATGGCACGATCCC
                                                                      Sequence 9083, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELLCOBACTER PYLORI
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :|||
5571 rProValTrpArgArgProGlyCysPro 5580
                                                                                                                                                                                                                                                                                                                                                                                                                                        1520 GCCGCAAAATCCTATCCTGCTGCCCA 1547
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ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 9083:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 206 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: Massachusetts
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
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US-10-335-977-9083
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Sequence 11657, A Sequence 14, Appl Sequence 14, Appl Sequence 74, Appl Sequence 58, Appl Sequence 41, Appl Sequence 42, Appl Sequence 42, Appl

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Sequence:

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Sequence 5462, Application US/10467657
; Sequence 5462, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
    APPLICANT: CHIRON SpA
    APPLICANT: FONTANA MATIA Rita
    APPLICANT: PONTANA MATIA Rita
    APPLICANT: MASIGNANI Vega
    APPLICANT: MONACI Elisabetta
    TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLBIC ACIDS
    FILE REFERENCE:
    CURRENT APPLICATION NUMBER: US/10/467,657
    CURRENT FILING DATE: 2001-02-12
    NUMBER: OF SEQ ID NOS: 9218
    SOFTWARE: SeqWin99, version 1.04
    SEQ ID NO 5462
    LENGTH: 5.25
1 US-11-096-568A-14646
1 US-11-096-568A-11657
1 US-11-169-232-14
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US-11-096-568A-20039
US-11-096-568A-17494
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US-10-510-386-30
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US-10-467-657-5462
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Best Local Similarity:
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US-10-467-657-5462
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   Sequence 5462, Ap
Sequence 1068, Ap
Sequence 2518, Ap
Sequence 2698, Ap
Sequence 1641, Ap
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               GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                               232119 seqs, 45477862 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Sequence 142, App Sequence 50, Appl Sequence 60, Appl Sequence 60, Appl Sequence 14, Appl Sequence 22, Appli Sequence 52, Appli Sequence 62, Appli Sequence 748, Ap Sequence 148, Ap Sequence 148, Ap Sequence 148, Ap Sequence 148, Ap Sequence 1864, A Sequence 2318, Appl Sequence 1984, Appl Sequence 28958, A Sequence 2071, Appl Sequence 2071, Appl Sequence 2071, Appl Sequence 2071, Appl Sequence 2071, Appl Sequence 2071, Appl Sequence 2071, Appl Sequence 2071, Appl Sequence 2073, Appl Sequence 2073, Appl Sequence 2073, A

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Matches:
Conservative:
Mismatches:
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/519,444
PRIOR PILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 09/504,629
PRIOR PILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-01-10
PRIOR PELING DATE: 2000-01-10
PRIOR PELING DATE: 1999-12-30
REMEATING DATE: 1999-12-30
REMEATING DATE: 1999-12-30
REMEATING PRIOR APPLICATION NUMBER: US 09/476,296
PRIOR FILING DATE: 1999-12-30
REMEATING PRIOR APPLICATION NUMBER: US 09/476,296
PRIOR FILING DATE: 1999-12-30
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SOFTWARE: FRASERQ FOR WINDOWS VERSION 4.0
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1037 ACAGACGCACTGGCAAAACTGGTGCAGGACGGCATAGACGTTACCGTCCTGACCAACTCG 1096
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218 AlabheAspPro---IleAlaSerProTrpIleVal---------Arg 229
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285 GluSerPheLeuAsnAspTrpValTyrMetGluAsnGlnAlaGlyAlaAlaAspGlyPhe 304
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PRIOR PELING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: 10/257,023
PRIOR APPLICATION NUMBER: 10/257,023
PRIOR FILING DATE: 2003-10-08
PRIOR FILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 2854
SSCPIMARE: Patentin version 3.3
LENGTH: 504
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CURRENT FILING DATE: 2005-01-28
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CHARBIT, ALAIN
DURANT, LIONEL
PEREZ-DIAZ, JOSE-CLAUDIO
BAQUERO, FERNANDO
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GARRIDO-GARCIA, PATRICIA
TIERREZ-MARTINEZ, ALBERTO
                                                           Sequence 2518, Application US/11045004
Publication No. US20060078901A1
GENERAL INFORMATION:
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US-11-045-004-2518
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COUVE, ELISABETH
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DEHOUX, PIERRE
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GOEBEI, WERNER
KREFT, JURGEN
KUHN, MICHAEL
NG, EVA
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HAUF, JORG
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APPLICANT: KARST, UWE
APPLICANT: ENTIAN, KARL-DIETER
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APPLICANT: ENTIAN, KARL-DIETER
APPLICANT: ENTIAN, KARL-DIETER
APPLICANT: HAFF, JONG
APPLICANT: NOSS, HAMUT
TITLE OF INVENTION: LIGTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
TITLE OF INVENTION: LIGTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
CURRENT APPLICATION NUMBER: US/11/045,004
CURRENT FILING DATE: 2003-08-11
PRIOR FILING DATE: 2003-08-11
PRIOR FILING DATE: 2002-10-08
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
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NUMBER OF SEQ ID NOS: 2854
SEQ ID NO 2698
LENGTH: 482
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GOMEZ-LOPEZ, NURIA
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CHARBIT, ALAIN
DURANT, LIONEL
PEREZ-DIAZ, JOSE-CLAUDIO
BAQUERO, FERNANDO
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GARRIDO-GARCIA, PATRICIA
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APPLICANT: FRANGEUL, LIONEL
APPLICANT: COUVE, ELISABETH
APPLICANT: RUSNIOK, CHRISTOPHE
APPLICANT: PSIHI, HAFIDA
APPLICANT: DEHOUX, PIERRE
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Alignment Scores: 3.79e-09 Length: 1970  Pred. No.: 250.50 Matches: 123 Score: 250.50 Matches: 69 Best Local Similarity: 24.5\$ Mismatches: 196 Query Match: 9.8\$ Indels: 115 DB: 9 No.: 24 US-10-665-990A-13 (1-1561) x US-10-821-234-1641 (1-1970)	Qy 108 TGGAAGAACGGACGGAAAGCCGTCATTTCAATACTTCCAAACCTGTCCTCGGACAACA 167	Qy 168 TCCTGCAAATCCGGCACCCCTCATAACAACGGGCTATCCGACATCTACCTGC 221	Qy 222	Qy 246 CCGCCGCGCCCTTATCGAATCTGCCGAACACGCCTCGATTTGCAATACTACATTT 305	Qy 306 GGCGCAACGACATTTCCGGCAGGCTGCTGTTCAACCTCATGTACCTTGCCGCAGAACGCG 365	Qy 366 GCGTGCGTACGCCTGCTGTTGGACGACAACACGCGGGGTTGGACGATCTCCTGC 425	Oy 426 TCGCCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCTACGCA 485	0y 486AATGGCGCGCACTCGGCTACCTGACCGACTTCCCCCGCCTCAACCGCCG 536 ::	Oy 537 TGCACAAATCCTTTACCGCCGCAACCAACCATACTCGGCGGACGAATATCG 596	Qy 597 GCGACGAATACTTCAAAGTCGGTGAGGACCACCGTTTTCGCCGACCTGGACATCCTCGCCA 656 :::	0
Qy         746 GGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAAACATCC 796	Oy 899 ATCAGCGACACCCCTGCAAAAGGACTCGACCGCGGCGCGCAAACCGCCGATTGCCGGG 958	Qy 959 AGGCTGCAAGACGCGCTCAAACAACAAGAAGGTCTATGTGGTTTCACCCTATTTC 1018 :::	Qy     1019 GTCCCTACAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGACGCATAGACGTT 1078       :::                  Db     341 IleProAspAlaSerLeuLeuGluAlaIleLysIleAlaAlaLeuSerGlyValAspVal 360	<pre>Qy 1079 ACCGTCCTGACCTACGCTACGGCGACCGACCGTGCCGCCGTCCATTCCGGCTACGTC 1138</pre>	OY 1139 AAATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCAT 1198	OY 1199 GCCGTCCCCGCACAAAGACAAAGGCCTGACCGGCAGCTCCGTAACCAGCCTGCATGCC 1258	OY 1259 AAAACCTTCATTGTGGACGCAAAGGCATCTTCATCGGCTCATTCAACCTCGACCCCGT 1318	OY 1319 TCCGCACGCTCAATACCGAAATGGCGTCGTCGAAAGCCCCCAAAATCGCAGAACAG 1378	Qy 1379 ATGGAGCGCACCCTCGCCGATACCACACCCGAATAC 1414 :::	Oy 1415 GCCTACGC 1423  Db 462 AlaLysArg 464	RESULT 5 US-10-821-234-1641  Sequence 1641, Application US/10821234  Publication No. US20050255114A1  Sequence 1641, Application US/10821234  Publication No. US20050255114A1  Setence 1641, And and and and and and and and and and a

US-10-665-990A-13 (1-1561) x US-11-096-568A-14646 (1-702)	73 CCTTCTCTGTTCATGTTCTTCATGGTTGCCCCCACTGGAAGAACGGACGG	133 TTTCAATACTTCCAAACCTGTCCT 156	157 CCTGGACAACATCCTGCAAATCCGGCACACCCCTCATAACAACGGGCTATCCGA 210	211 CATCTACCTGCTCGACGACCCCCACGAAGCCCTTGCCGCGCCGCCCCTTATCGAATC 270	271 TGCCGAACAGCCTCGATTTGCAATACTACATTTGGCGCACGACATTTCCGGCAGGCT 330	GCTGTTCAACCTCATGTACCTTGCCGCAGAACGCGGCGTGCGCGT			154 AlaAspArgArgAlnLeuArgAlaArg 162	478 CCTACGCAAATGGCGCGCACTCGGCTACCTGACCGCCCCCCCC	538 GCACAACAAATCCTTTACCGCCGACAACCG	568CGCCACCATACTCGGCGGACGCAATATGGCGACGAATA 606		607 CTTCAAAGTCGGTGAGGACACCGTTTTCGCCGACCTGGACATCCTCGCCACCGGCAGCGT 666	GGTCGGCGAAGTATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAACGC		727 CAGGGGATCATCGGCAGCGGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGA 786	247 HisTrpargAlaala 251	787 CGAAACATCCAGACACGCGCTCCTGCGCGAAACCGTCGAACAGTCGCCCCTCTA 846	252 ArgAlaLeuArgAspArgAlaProArgProValLeuArgAlaArgArgValArg 269	CCAAAAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTGATCAGCGA	rronigelyrroneuelyargargargelyeliargargrionigheuneuelarig	907 CACCCTGGGGGGACGCGCGACGCGCAACGCGCGATGCGGGGGGCTGCA 966	967 AGACGCGCTCAAACAGCCCCGAAAAAGCGTCTATCTGGTTTTCGTCCCTAC 1026	:::     309 ArgArgProArgAspArgArgProLeuArgLeuArgArgAlaAla 323
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-----ACTTCAAAGTTCGGGGGACACCGTTTTCGCCGACCTGACATCGTCGCCACG 659
ArgAlaSerAlaAlaThrSerArgThrProProSerProArgSerThrSerSerProThr 217
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Mismatches:
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Matches:
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                                                                                          NAME/KEY: misc_feature
LOCATION: (1)..(493)
OTHER INFORMATION: Ceres Seq.
US-11-096-5688-11657
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248.00
35.5%
23.9%
8.7%
SEQ ID NO 11657
LENCTH: 493
TYBE: PRT
ORGANISM: Triticum aestivum
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Best Local Similarity:
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Pred. No.:
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US-11-096-568A-11657

US-11-096-568A-11657

Sequence 11657, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1552PUS2

CURRENT APPLICATION UNMERE: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471
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| ArgArgAlaProGlnAlaArgArgGlyArgValGlyAspGlyValGlyGlyArgAlaGly 439
                                                                                                                                                                                                                                                                      |||::: ||||||| ArgHisHisArgGlyLoughyCysAlaArgPro----ProGlyGlyValGlnAla 399
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                                                                                                                     440 LeuLeuLeuLeuProProValGluArgValGlyGlyArgGlyAspGlyArgGlyGlyGly
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                       1027 AAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGA--
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ZIP: 02140  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/11/169,232 FLING DATE: 28-Jun-2005 CLASSIFICATION PATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2001	APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991 APPLICATION NUMBER: US 07/546,114 FILING DATE: 29-UN-1990 APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989 ATTOREY/AGENT INFORMATION: NAME: CSETY, LUARN REGISTRATION NUMBER: 31,822 ATTOREY/AGENT INFORMATION: TELEREANCE/OCKET NUMBER: G1 5190 TELEFRANCATION INFORMATION: TELEFRANCE (617)876-1170 TELEFRANCE (617)876-1170 SEQUENCE CHARACTERISTICS: INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: TYPE: amino acids TYPE: amino acids TYPE: amino acids TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 14:	Alignment Scores:     Pred. No.:         247.50	Qy         249
	Db 285	Db 330	RESULT 8 US-11-169-232-14 ; Sequence 14, Application US/11169232 ; Publication No. US20060025570A1 ; GENERAL INFORMATION:

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Length:
Matches:
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FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cserr, Luann
RAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0,
                 1473 GAAAAACCTACCCGAACGAACCCGAAG 1499
                                      ::::::|||
LysGluProAlaProThrThrProLys 572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                       Sequence 84, Application US/11169232;
Publication No. US/20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                  CITY: Cambridge
STATE: Massachusetts
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SEQUENCE CHARACTERISTICS:
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247.50
35.2%
26.5%
8.7%
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                       US-11-169-232-84
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515 ProThrThrLeuLysGluProAlaPro-----ThrThrProLys-----Lys 528
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ThrThrSerAspLysProAlaProThrThrPro---LysGlyThrAlaProThrPro 563
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                                                                                                                                            279 ThrProLysGluProAlaProThrAlaProLysLysProAlaProThrThrProLysGlu 298
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319 ThrProLysGluProAlaProThrThrLysSerAlaProThrThrLysGluPro 338
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| GluProThrProThrThrProLysGluProAlaProThrThrLysGluProAlaProThr
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                                  501 GCTACCTGACCGACTTCCCCCGCCTCAACCGCCGCATGCACAACAAATCCTTTACCG---
                                                                                                                                                                             ---GCGCCACCATACTCGGCGGACGCAATATCGGCGACGAATACTTCAAAGTCGGTGAGG
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CCAAACCTGTCCTCCTGGACAACATCCTGCAAATCCGGCACACCCCTCATAACAACGGGC 203
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           Version #1.25
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Mismatches:
Indels:
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-DAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1989
                                                                                                                                ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
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us-10-665-990a-13.rapbn

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---CCGTCCATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCATCAAAC 1175
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                                                                                                                       -----ACACCCCTGCAAAAGGACTCGACCGCGACCGCCAAACCGC 947
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LysGluProAlaProThrThrPro-----LysGluThrAlaProThrThrProLysLys 489
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531 AlaProThrThrProLysAlaAla---AlaProAsnThrProLysGluProAla----
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Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte StimmumBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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COUNTRY: U.S.A.
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US-11-169-232-58
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404 AlaProThrThrLysSerAla-------ProThrThrProLysGluPro 418
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275 ProLysGluProAlaProThrThrLysGluProAla---
                                                                                                                                                                                                                                                                                                                   US-10-665-990A-13 (1-1561) x US-11-169-232-74 (1-1038)
                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                 Indels:
                                                                                                                         74:
                                                                                                                                                                                                                                                                                   Gaps:
                                                                    TYPE: amino acid
TOPOLLGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-11-169-232-74
TELEFAX: (617)876-5851
KMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino acids
                                                                                                                                                                                          5.5e-09
247.50
35.2%
26.5%
8.7%
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Best Local Similarity:
Query Match:
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                   INFORMATION
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                               369 ThrThrIleLysSerAlaProThrThrProLysGluProAlaProThrThrThrLysSer 388
                                                                                                                                        CCGGCAGGCTGCTGTTCAACCTCATGTACCTTGCCGCAGAACGCGGCGTGCGCGTACGCC 380
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665 AlabroThrThrProLysAlaAla---AlaProAsnThrProLysGluProAla---- 681
CCCGCGCCCCTTATCGAATCTGCCGAACACACACCCTCGATT 290
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518 ThrProLysGluProAlaProThrThrThrLysSerAlaProThrThrLysGluPro
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|SerProThrThrLys------GluProAlaProThrThrProLysGluPro
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                                                                                                                    Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.25
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Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Ve;
RENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Unn-2005
CLASSIFICATION: «UNKNOWN»
OR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-DAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                           ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                             Sequence 104, Application US/11169232 Publication No. US20060025570A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1140 amino acids
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                    APPLICANT: Turner, Katherine
                                                                                                         Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 104:
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                                                                                                                                                                                                                                                                                  STATE: Massachusetts
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Query Match:
DB:
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RESULT 12
US-11-169-232-104
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384 ThrProLysGluProAlaProThrThrLysSerAlaProThrThrThrLysGluPro 403
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Matches:
Conservative:
Mismatches:
Indels:
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                                                             NO: 44:
 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                      247.50
35.2%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                       CCTACCGCGTTACCCTCGACAAACACCGCCTGCAATGGCACGATCCCG---CCACCC 1472
                                                                                                                                                                                                                              AAAGCCCCAAAAATCGCAGAACAGATGGAGCGCACCCTCGCCGATACCACACCCCGAATACG 1415
                                                                                                                                                  GCTCATTCAACCTCGACCCCCGTTCCGCACGGCTCAATACCGAAATGGGCGTCGTCATCG 1355
1176 TCTACGAGCTGCAACCCAAGCGTCCCCGCCACAAAGACAAAGGCCTGACCGGCA 1235
                                                                                                 728 ProAlaProLysGlu------LeuAlaProThrThrThrLysGluProThrSer 743
                                                                                                                                                                                                                                                                                                                                             744 ThrThrSerAspLysProAlaProThrThrPro---LysGlyThrAlaProThrThrPro 762
                     1236 GCTCCGTAACCAGCCTGCAAAAACCTTCATTGTGGACGGCAAACGCATCTTCATCG
                                                                                                                                                                                        714 ProThrThrLeuLysGluProAlaPro-----ThrThrProLys-----Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Turner, Katherine
Clark, Stephen C.
Clark, Stephen C.
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPENATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
FILING DATE: 16-Apr-1091
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,119
FILING DATE: 29-DEC-1989
FILING DATE: 29-DEC-1989
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                 1473 GAAAAACCTACCCGAACGAACCCGAAG 1499
                                                                                                                                                                                                                                                                                                                                                                                                                       763 LysGluProAlaProThrThrProLys 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 44, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1270 amino acids
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INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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COUNTRY: U.S.A.
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                                                                                                                                                  1296
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FILING DATE: 28-Jun-2005 CLASSIFICATION: <unknown> PRIOR APPLICATION DATA:  APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002 APPLICATION NUMBER: US 07/646,114 FILING DATE: 19-JAN-1990 APPLICATION NUMBER: US 07/546,114 FILING DATE: 29-JUN-1990 APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DGC-1989 APPLICATION NUMBER: US 07/390,901 FILING DATE: 29-DGC-1989 APPLICATION NUMBER: US 07/390,901 FILING DATE: LS-DGC-1989 APPLICATION NUMBER: US 07/390,901 FILING DATE: CS-TX, LUADN MAME: CS-TX, LUADN ATTORNEY/AGENT INFORMATION: TELECOMMUNICATION INFORMATION: TELEFRANCE/DOCKET NUMBER: GI 5190 TELEFRANCE/LOCKET ON OFFICE OF</unknown>	Alignment Scores: 5.67e-09 Length: 1311  Pred. No.: 247.50 Matches: 135 Score: 25.2\$ Matches: 44 Best Local Similarity: 26.5\$ Mismatches: 205 Query Match: 11 Gaps: 29 Bs: 14 CCAAACCTGTCCTGGACAACATCCGCACACCCTCATAACAACGGGC 2	144 CCAMACTICICICICANATICLICANATICUSCANATICUSCANATICUS AND CONTROL OF THE CONTROL	291 296 321 381 381 329 441 346 501 365 558
	Db 561 GluproAlaProThrThrProLysGluThrAlaProThrProLysGlyThrAla 579  Qy 1296 GCTCATTCAACCTCGACCCCGTTCCGCACGGCTCATACGAAATGGCCGTCGTCATCG 1355  Db 580 ProThrThrLeuLysGluProAlaProThrThrProLysLys 593  Qy 1356 AAGCCCCAAAATCGCAGAAGGAGGCACCCTCGCCGATACCCGAATACG 1415  Db 594 ProAlaProLysGluLeuAlaProThrThrLysGluProThrSer 609  Ov 1416 CCTACCGCGTTACCCTCGAAAACACAAACCGCTGCAATGGCACCACTCCGCCACCC 1472	1416 CTACCGCGTTACCCTCGACAAACACCTGCAATGCGGACGACCGGCGGGACCGGGGGACGCGGGGGGGG	Publication No. US20060025570A1 GENERAL INFORMATION: Clark, Stephen C. Clark, Stephen C. Gacobs, Kenneth Hewick, Rodney M. Geener, Thomas G. TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143 CORRESPONDENCE ADDRESS: ADDRESSEE: Genetics Institute, Inc. STREET: 87 cambridge Park Drive CITY: Cambridge Park Drive CITY: Cambridge STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02140 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/11/169,232

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| SSB GlubroThrProThrThrProLysGluProAlaSerThrThrProLysGluProThrPro
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                                                                             Clark, Stephen C.
Jacobs, Kanneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURREMY APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/11/169,232

FILING DATE: 28-Unn-2005

CLASSIFICATION: Unknown>
PRIOR APPLICATION OFF:

APPLICATION NUMBER: US/10/124,557

FILING DATE: 16-AP-2002

APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-UN-1990

APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-EC-1989

APPLICATION NUMBER: US 07/57,196

FILING DATE: 29-EC-1989

APPLICATION NUMBER: US 07/57,196

APPLICATION NUMBER: US 07/57,196

APPLICATION NUMBER: US 07/57,196

APPLICATION NUMBER: US 07/57,196

APPLICATION NUMBER: US 07/57,196

APPLICATION NUMBER: US 07/590,901

FILING DATE: 08-AUG-1889
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Matches:
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 142:

US-11-169-232-142
                                                                                                                                                                                                                                          ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1313 amino acids
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                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
       Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Kathe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
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247.50
35.2%
26.5%
8.7%
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Best Local Similarity:
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ThrProLysGluProAlaProThrAlaProLysLysProAlaProThrThrProLysGlu 404
                                                                                                                                                                    TATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAACGCCACGCGCATCA 737
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                                                                                                                                                                                                                                                                                                                                    797
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                                                ---GCGCCACCATACTCGGCGACGCAATATCGGCGACGAATACTTCAAAGTCGGTGAGG 623
                                                                                                                                         ACACCGTTT-----TCGCCGACCTGGACATCCTCGCCACCGGCAGCGTCGTCGGCGAAG 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------ACACCCTGCAAAGGACTCGACCGCGACCGCCGCAAACCGC 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572 AlaProThrThrProLysAlaAla---AlaProAshThrProLysGluProAla----
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                                                                                           405 ProalaProThrThrProLysGluProAlaProThrThrThysGluProSerProThr
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; Sequence 142, Application US/11169232
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                                                           948 CGATTGCCGGGAGGCTGCAAGACGCGCTCAAACAGCCCCGAAAAAGCGTCTATCTGGTTT 1007
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   516 LysGluProAlaProThrThrPro-----LysGluThrAlaProThrThrProLysLys
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                                                                                     Version #1.25
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Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Fac
CORRESPONDENCES: 143
CORRESPER: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
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FILING DATE: 28-Jun-2005
FILING DATE: cardin-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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673 LysGluProAlaProThrThrProLys 681
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COUNTRY: U.S.A.
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|SerProThrThrLys------GluProAlaProThrThrProLysGluPro 478
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     ProAlaProThrThrProLysGluProAlaProThrThrThrLysGluProSerProThr 433
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454 AlaProThrThrLysSerAla------ProThrThrProLysGluPro
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LysGluProAlaProThrThrProLys 687
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Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                               NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REPERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                             5.67e-09
247.50
35.2%
26.5%
                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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1008 CACCCTATTTCGTCCCTACAAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGACG 1067
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          CCGCCAGGCTGCTGCTCAACCTCATGTACCTTGCCGCAGAACGCGGCGTGCGCGTACGCC 380
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                                                                          TGCTGTTGGACGACACACACGCGCGGGTTGGACGATCTCCTGCTCGCCCTCGACAGCC
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Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
NY APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-AP-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <UNKNOWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617)876-1170
TELEPRA: (617)876-5851
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                 STATE: Massachusetts
COUNTRY: U.S.A.
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247.50
35.2%
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                                                                                                                     CITY: Cambridge
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Best Local Similarity:
Query Match:
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1296 GCTCATTCAACCTCGACCCCGCACGCTCAATACCGAAATGGGCGTCGTCATCG 13 630 ProThrThrLeuLysGluPrOAlaProThThrThrProLysLys 64 1356 AAAGCCCCAAAATGGAGAACAGATGGAGCGCACCTCGCCGATACCACCCGAAATGGAGGGGACCCTCGCCGATACCACCCGAAAACGATGAACAGATGGAGCGCACCTCGCCGATACCACCCGAATGGAGAGCGCACCTCGCCGATACCACCCGAATGGAGAGCGCACCTCGCCGATACCTCGAATGGACAGAACCGCCTGCCAAAAAACAACCGCCTGCAATGGCACGATCCCGGCCACCC 14 1116 CCTACCGCGTTACCCTCGACAAAACACCACCCCGCAATGGCACGATCCCGGCCACCC 14 1116 CCTACCGCGTTACCCTCGACAAAACACAACCGCCTGCAATGGCACGATCCCGGCCACCC 14 1111	DD 660 InfinfSerAspLysPtOAlaProinfInfPtOLysGlyInfAlaProinfInfPtO 6/8 Qy 1473 GAAAAACCTACCCGAACGAACCCGAAG 1499 Db 679 LysGluProAlaProThrThrProLys 687	RESULT 19 US-11-169-232-48 ; Sequence 48, Application US/11169232 ; Publication No. US20060025570A1 ; GENERAL INFORMATION: ; APPLICANT: Turner, Katherine	Clark, S Jacobs, Hewick, Gesner, NVENTION:	NUMBER OF SEQUENCES: 143 CORRESPONDENCE ADDRESS: ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive	CITY: Cambridge  STATE: Massachusetts  COUNTRY: U.S.A.  ZIP: 02140	COMPUTER REALABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: PatentIn Release #1.05	CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/11/169,232  FILING DATE: 28-Jun-2005	PRIOR APPLICATION DATA:  APPLICATION NUMBER: US/10/124,557  FILING DATE: 16-Apr-2002	APPLICATION NUMBER: US 07/643,502 	APPLICATION NUMBER: US 07/457,196 ; FILING DATE: 29-DEC-1989 ; APPLICATION NUMBER: US 07/390,901 ; FILING DATE: 08-AUG-1989	HILDRAKITAGENT INCHMATION: HAMBER: SERIK LUGAN REGISTRATION NUMBER: 31,822 REFERENCE/DOCKET NUMBER: GI 5190	TELECOMMUNICATION: TELEPHONE: (617)876-1170 TELEFRAX: (617)876-5851 TELEFRAX: (617)876-5851 TIFORMATION FOR SEQ ID NO: 48:		; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 48: US-11-169-232-48	Alignment Scores: 5.69e-09 Length: 1354

FILING DATE: 29-JUN-1990	Oy 144 CCAAACCTGTCTCCTGGACAACATCCGGGACACCCCTCATAACAACGGC 203	
	1416 CCTACCGCGTTACCCTCGACAACACAACCGCCTGCAATGGCACCGCCACCC 1472    :::	ILT 20 IL.169-232-40 IL.169-232-40 IL.169-232 guence 40, Application US/11169232 publication No. US20060025570A1 GENERAL INFORMATION: Clark, Stephen C. Jacobs, Kenneth Hewick, Rodney M. Gener, Thomas G. TITLE OF INVENTION: Megakaryocyte Stimulating Factors ORRESPONDENCE ADDRESS: ADDRESSE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: CambridgePark Drive CITY: CambridgePark Drive CITY: CambridgePark Drive CONTRY: U.S.A. CONTRY: U.S.A. CONTRY: U.S.A. COMPUTER: 1BM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-App. 2002 RIUNG DATE: 16-App. 2002 FILING DATE: 16-App. 2002 FILING DATE: 16-App. 2002 FILING DATE: 16-App. 2002 FILING DATE: 16-App. 2002 FILING DATE: 16-App. 2002 FILING DATE: 16-App. 2002 FILING DATE: 18-AJM-1991 APPLICATION NUMBER: US 07/546,114

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --TTTGGCGCAACGACATTT 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-665-990A-13 (1-1561) x US-11-169-232-52 (1-1363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATE:

APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-APL-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/546,116
FILING DATE: 29-BC-1889
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                          ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <UNKNOWD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: CSErr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617)876-5851
                                                                                                         STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCE CHARACTERISTICS
LENGTH: 1363 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 52
                                                                                                                                                        ZIP: 02140
COMPUTER READABLE FORM:
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247.50
35.2%
26.5%
8.7%
                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                      CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCAATACTACA-
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Pred. No.:
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NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1176 TCTACGAGCTGCAACCCAACCATGCCGTCCCCGCCACAAAGACAAAGGCCTGACCGGCA 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1236 GCTCCGTAACCAGCCTGCATGCCAAAACCTTCATTGTGGACGGCAAACGCATCTTCATCG 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1296 GCTCATTCAACCTCGACCCCCGTTCCGCACGGCTCAATACCGAAATGGGCGTCGTCATCG 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               948 CGATTGCCGGGAGGCTGCAAGACGCGCTCAAACAGCCGGAAAAAGCGTCTATCTGGTTT 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1008 CACCCTATTTCGTCCCTACAAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGACG 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     652 GluProAlaProThr---ThrProLysGluThrAlaProThrThrProLysGlyThrAla 670
                                                                                                                                                                             525
                                                                                                                                                                                                                                                     -----ProThrThrProGluLysProAlaProThrThrProGlu-----GluLeu 605
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                                            737
                                                                                                                                                                                                                                                                                                                  849 AAAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTGATCAGCG--- 905
                                                                                                                                                                                                                                                                                                                                              906 ------ACACCCTGCAAAAGGACTCGACGCCGCGCCGCAAAACGC 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606 AlaProThrThrProGluGluProThr------ProThrThrProGluGluPro 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 ThrProLysGluProAlaProThrThrLysSerAlaProThrThrLysGluPro 494
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622 AlaProThrThrProLysAlaAla---AlaProAsnThrProLysGluProAla-----
                                            678 TATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAACGCCACGCCATCA
                                                                                        -----ProThrThrProLysGluPro
                                                                                                                                                                                                                                                                                                                                                                                                                                     563 LysGluProAlaProThrThrPro-----LysGluThrAlaProThrThrProLysLys
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-----ThrThrProGluLysLeuAla------
                                                                                                                                     TCCGCAGCGGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAAACATCCA
                                                                                                                                                                             510 SerproThrThrThrLys------GluProAlaProThrProLysGluPro
                                                                                                                                                                                                                         -----GACACGCGCTCCTGCGCTACCGCGAACGTCGAACAGTCGCCCTCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
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671 ProThrThrLeuLysGluProAlaPro-----ThrThrProLys-
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Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Renneth
Hewick, Rodney M.
Geener, Thomas G.
                                                                                        495 AlaProThrThrThrLysSerAla-
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US-11-169-232-52
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Qy         1356 AAAGCCCCAAAATCGCAGAACAGATGGAGCGCACCCTGCCGATACCACCCGAATACG 1415           Db         687 ProAlaProLysGluLeullaProThrThrLysGluProThrSer 702           Qy         1416 CCTACCGCTTACCCTCGACAACACACACCCTGCAATGGCACGATCCGCCCACCC 1472           Db         703 ThrThrSerAspLysProAlaProThrThrProLysGlyThrAlaProThrThrPro 721           Qy         1473 GAAAAACCTACCGAACGAACCGAAG 1499           122 LysGluProAlaProThrThrProLys 730		APPLICANT: Turner, Katherine Clark, Stephen C. Jacobs, Kenneth Hewick, Rodney M. Genner, Thomas G. TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143	CORRESPONDENCE ADDRESS:  ADDRESSE: Gnetics Institute, Inc.  STREET: 87 CambridgePark Drive  CITY: Cambridge  STATE: Massachusetts	COMPUTER READABLE FORM:  COMPUTER READBY disk  COMPUTER: Floppy disk  COMPUTER: Ploppy disk	CURRENT APPLICATION DATA:  CURRENT APPLICATION DATA:  APPLICATION NUMBER:  FILING DATE: 28-011/169,232  CLASSIFICATION: <a href="checkbox">checkbox</a> CLASSIFICATION: <a href="checkbox">checkbox</a> CLASSIFICATION: <a href="checkbox">checkbox</a>	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US/10/124,557 ; FILING DATE: 16-Apr-2002 ; APPLICATION NUMBER: US 07/643,502	; FILING DATE: 18-JAN-1991 ; APPLICATION NUMBER: US 07/546,114 ; FILING DATE: 29-JUN-1990 ; APPLICATION NUMBER: US 07/457,196 ; FILING DATE: 29-DEC-1000	FILING DATE: US 07/390,901  FILING DATE: 08-AUG-1989  ATTONEY AGENT INFORMATION:  NAME: Geory Lusan	REGISTRATION NUMBER: 31,822 REFERENCE/DOCKET NUMBER: GI 5190 TELECOMMUNICATION:	TELEBRHOUE: (61/)8/6-11/0 TELEBRAX: (61/)8/6-5851 ; INFORMATION FOR SEQ ID NO: 2: ; SEQUENCE CHARACTERISTICS:	;	
	GluProThrFroThrThrProLysGluProAlaProThrThrLysGluProAlaProThrCGACAACC ThrProLysGluProAlaProThrAlaProLysBroAlaProThrThrProLysGlu	567GGGCGCACCATATTGGGGGGGGGGATATGGGCGATACTTGAAGTGGGTGAGG 623  457 ProAlaProThrThrProLysGluProAlaProThrThrThrLysGluProSerProThr 476  624 ACACCGTTTTGGCGGACGTGGACATCCTCGCACGGGGGGGGGG	678 TATCGCACCACTTCGACCGCTACTGGGCAAGCCATTCCGCCACAACGCCACGGGATCA 737                ::: 497 AlaProThrThrThrThrLysSerAlaProThrThrProLysGluPro 511 738 TCCGAGGGCAACATCGGCAAGGGTCTTTCAAGCAATCGATACAAACAA		528 AlabroThrThrProLysbroAlabroThrThrProLysGluBroAlabroThrThr 547 849 AAAAATACAGACGGACGCATGGCAGAGCGTCCAAACCGCGCTGATCAGCG 905	906	948 CGATTGCCGGGAGGCTGCAAGACGCCTCAAAAAAGCGTCTATCTGGTTT 1007 	1008 CACCCTATTTCGTCCCTACAAAATCCGGCACAGACGCACTGGCAGAAACTGGTGCAGGACG 1067 ::::::::::::::::::::::::::::::::::::	1068 GCATAGACGTTACCGTCCTGACCAACTCGCTACAGGCGACGTTGCCG 1118 	1119CCGTCCATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGCATCAAAC 1175     :::      624 AlaProThrThrProLysAlaAlaAlaProAsnThrProLysGluProAla 640		1236 GCTCCGTAACCAGCTGCAAACCTTCATTGTGGACGCAACGCATCTTCATCG 1295  654 GluProAlaProhrThrProLysGluThrAlaProThrThrProLysGlyThrAla 672  1296 GCTCATTCAACCTCGACCCCGTTCCGCACGGCTCAAAACCGAAATGGGCGTCGTCGTCCGTC

09 1199	COUNTRY: U.S.A.  ZIP: 02140  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.25  CURRENT APPLICATION DATA: APPLICATION NUMBER: US/11/169,232  FILING DATE: 28-Jun-2005  CLASSIPICATION: <unknown-> PRIOR APPLICATION NUMBER: US/10/124,557  FILING DATE: 16-Apr-2002  APPLICATION NUMBER: US 07/643,502  FILING DATE: 18-JAN-1991  APPLICATION NUMBER: US 07/546,114  FILING DATE: 29-JUN-1990  APPLICATION NUMBER: US 07/457,196  FILING DATE: 29-DEC-1999  APPLICATION NUMBER: US 07/457,196  FILING DATE: 29-DEC-1999  APPLICATION NUMBER: US 07/457,196  FILING DATE: 29-DEC-1999</unknown->
11   Caps: 29	T38 TCCGCAGCGGCAACATCGGCAACGGTCTTCAAGCACTCGGATACAACGACGAAACATCCA 797

us-10-665-990a-13.rapbn

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948 CGATTGCCGGGAGGCTGCAAGACGCGCTCAAACAGCCCCGAAAAAGCGTCTATCTGGTTT 1007
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             --ProThrThrProLysGluPro 552
                                                                                                                                                                                             849 AAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTGATCAGCG---
                                                                                                                                                                                                                                589 ProLysGluProAlaProThrThrThr-----LysLysProAlaProThrAlaPro
                                                                                                                                                                                                                                                                       ------ACACCCTGCAAAAGACTCGACCGCGACCGCCAAACCGC
                                                                                                                                                                                                                                                                                              ||||||||
LysGluProAlaProThrThrPro-----LysGluThrAlaProThrThrProLysLys
                                                                                 SerProThrThrLys------GluProAlaProThrThrProLysGluPro
                                                                                                                      -----GACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGTCGCCCCTCTACC
                                            TCCGCAGCGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAAACATCCA
                                                                                                                                                                                                                                                                                                                                                                                 624 LeuThrPro--------ThrThrProGluLysLeuAla-----
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569 AlaProThrThrProLysLysProAlaProThrThrProLysGluProAlaProThrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             695 GlubroAlaProThr -- ThrProLysGluThrAlaProThrThrProLysGlyThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1473 GAAAAACCTACCCGAACGAACCCGAAG 1499
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763 LysGluProAlaProThrThrProLys 771
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CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5700, Application US/10467657 Publication No. US20050260581A1 GENERAL INFORMATION:
           538 AlaProThrThrThrLysSerAla--
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APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
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|ThrbrolysGluProAlaProThrThrThrLysSerAlaProThrThrLysGluPro 537
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Matches:
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Mismatches:
Indels:
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                                                                               5190
                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INPORMATION:
NAME: CSET, LUADIN
REGISTRATION NUMBER: 31,822
REFERENCE/OCKET NUMBER: GI 51
TELECOMMUNICATION:
TELEPHONE: (617)876-1170:
                                                                                                                                                                                      LENGTH: 1404 amino acids
                                                                                                                             TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
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247.50
35.2%
26.5%
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TOPOLOGY: linear
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is Sequence 7448, Application US/10467657

is Sequence 7448, Application US/10467657

is Dublication No. US20050260581A1

is GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: FONTAN Maxia Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNANI Vega

APPLICANT: MASIGNANI Vega

APPLICANT: MONACIE Bisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT APPLICATION NUMBER: GB-0103424.8

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR PILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SEQ ID NO 7448

SEQ ID NO 7448

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222 ArgArgHisArgHisCySArgArgGlnThrAlaAlaAlaGluIleHisThrAspValAla 241
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21 GluGlnArgIleArgAsnAlaAsnValGlyGlySerIleProPheSerGlyThrAsnThr
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SEGWIN99, version 1.04
SEQ ID NO 5700
LENGTH: 430
                                                                                                                                                        ) ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5700
                                                                                                                                                                                                                                                              96-09
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25.9%
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Sequence 7133, Application US/11079463
Publication No. US20060073161A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/128,705
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 7133
LENGTH: 503
                                                                                                                                                   1288 CITCAICGGCTCAITCAACCICGACCCCCGTTCCGCACGGCTCAAIACCGAAAIGGGCGI 1347
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                                                  GACCGGCAGCTCCGTAACCAGCCTGCATGCCAAAACCTTCATTGTGGACGCAAACGCAT 1287
                                                                                                                                                                                   323 AspHis-----ArgArgGlnAlaAlaIleSer-------GlnThrGln 334
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303 HisAspGlySerHisAlaAlaArgProProGlnAsnArgGlnHisHisArgAlaAlaPro 322
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81 ValPheTyrPhePhePhe-------GlyArgSerGlnArgArgGluLysIlelle 96
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| 222 ArgArgHisArgHisCysArgArgGlnThrAlaAlaAlaGluIleHisThrAspValAla 241
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Oy 1237 CTCCGTAACCAGCCTGCAAACCTTCATTGTGGA	RESULT 27 US-10-873-528-109 S-10-873-528-109 Publication No. US20050276814A1 GENERAL INFORMATION: APPLICANT: Microbial Technics Limited APPLICANT: Gilbert, Christophe FG APPLICANT: Hansbro, Philip M TITLE OF INVENTION:	FILE REFERENCE: PWC/P21129WO ; CURRENT APPLICATION NUMBER: US/10/873,528 ; CURRENT FILING DATE: 2004-06-23 ; PRIOR APPLICATION NUMBER: US/09/769,787 ; PRIOR FILING DATE: 2001-01-26 ; PRIOR FILING DATE: 1998-03-77 ; PRIOR FILING DATE: 1998-03-27 ; PRIOR FILING DATE: US/60/125164	PRIOR FILING DATE: 1999-03-19 NUMBER OF SEQ ID NOS: 388 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 109 LENGTH: 1236 TYPE: PRI ORGANISM: Streptococcus pneumoniae US-10-873-528-109	Alignment Scores:  Pred. No.:  Score:  Score:  Percent Similarity:  Best Local Similarity:  Query Match:  9 Gaps:	US-10-665-990A-13 (1-1561) x US-10-873-528-109 (1-123- Qy 126 GCGTCATTTCAATACTTCCAAACCTGTCCTGGACA- Db 551 AlaSerAlaSerIleSerAlaSerGluSerAlaSerThr.			Qy 357 CAGAACGCGGCGTGCGCGTACGCCTGCTGGACGACACACAC	Qy 474 TCGTCCTACGCAAATGGCGCGCACTCGGCTACCTGACCG
181 GCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACGACGCCCCCACGAAGC 240  137 AlaPhe - ProPheGluGlyAsnArgValAspileTyrThrGlyGlyTyrSerLy 154  241 CCTTGCCGCCCGCCGCCCCTTATCGAATCTGCCGAACACAGCCTCGATTTGCAATACTA 300  154 SLeuGlnAlaLeuLeuArgGluLeuGlnLySAlaArgLeuHisIleHisMetGluTyTY 174  301 CATTTGGCGCAACGACATTTCCGGCAGCTGCTTCAACCTTGCCGCAGA 360  11	ACGCGCGTGCCGCTGCTGTTGGACGACAACAACACGGCGGGTTGGACGATCT	481 ACGCAAATGGCGCACTCGGCTACCTGACCGACCCCCCGCCTCAA 528	CAATATCGCCGACGAATACTTCAAAGTCGGTGAGGACACCGTTTTCGCCGACCTGGACAT        : : : :         : :	GGCAAGCCATTCCGCCCACAAGGCCATCCGCAGGGGGCGCAAGGGG ::::::    :::      :::	823 AACCGTCGAACAGTCGCCCTCTACCAAAATACAGACGGACGCATCGACTG 876  826 NILeValThrSerGluProlieGlyProTrpLySGluIleMetGlnGly342  877 GCAGAGCGTCCAAACCCGCCTGATCAGCGACCCCTGCAAAAGGACTCGACGGGCGG 936	342 342 937 CCGCAAACCGCCGATTGCCGGGAGGCTGCAAGACGCCTCAAACAGCCCGAAAAAGCGT 996 1	CTATCTGGTTTCACCCTATTTCGTCCCTACAAAATCCGGCACAGGCACTGGCAAAACT		412 IlYrrnelyrbys
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ACGGCAAACGCATCTTCATCGG 1296
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hrSerAlaSerGluSerAlaSer 570
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AspAspMetLeuSerThrValGl 435
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luSerAlaSerThrSerAlaSer 590
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heGluValAsnAlaPheMetTy 455
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σ (	Db 997 nValLeuAlaProGlnProGlnProValArgGlnProGlnGlnValSerGlnAr 1017 Qy 1506 TȚTGGAAACGCATCGCÇGAAAATÇCȚATC 1536
	Db 1017 gLeuAsnArgHisGlnArgValArgProLeu 1027
594 TCGGCGACGAATACTTCAAAGTCGGTGAGACACCGTTT	RESULT 28 US-11-06-568A-14593 ; Sequence 14593, Application US/11096568A ; Publication No. US20060048240A1
633TCGCCGACCTGGACATCCTCGCCAGCGGCGCGCGGAAGTATCGC 683 731 AlaSerGluSerAlaSerThrSerAlaSerAlaSerAlaSerAlaSerAlaSerAlaSer 750	; GENERAL INFORMATION: ; APPLICANT: Alexandrov, Nickolai et al. ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide ; TITLE OF INVENTION: Therby
684 ACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAACGCCACGCGCATCATCCGCA 743 551 AlaSerThrSerAlaSerAlaSerAlaSerThrSerThrSerAlaSerAlaSerThrSer 770	; FILE REFERENCE: 2750-1592PUS2; CURRENT APPLICATION NUMBER: US/11/096,56BA; CURRENT FILING DATE: 2005-04-01; NUMBER OF SEQ ID NOS: 34471
744 GCGGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGAAGAT 794    :::       771 AlaSerAlaSerAlaSerThrSerAlaSerAlaSerIleSerAlaSerGluSer 790	; SEQ ID NO 14593 ; LENGTH: 758 ; TYPE: PRT ; ORGANISM: Zea mays subsp. mays
795 CCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGTCGCCCCTCTACCAAAAAA 854	; FEATURE: ; NAME/KEY: misc feature ; LOCATION: (1).7(758) ; CLOCATION: (1).7(758) ; OTHER INFORMATION: Ceres Seq. ID no. 11049133
	41500
C 97	241.50 241.50 milarity: 30.6% Similarity: 23.0%
10	11 Gaps: .0A-13 (1-1561) x US-11-096-568A-14593 (1-7
GCACAGACGCACTGGCAAAACTGGTGCAGGACGGCATAGACGTTACCGTCCTGACCAACT    ::	Oy 160 GGACAACATCCTGCAAATCCGGCACCCCTCATAACAACGGGCTATCCCACATCTACCT 219
GCTACAGGCGACCGACGCTGCCGCCGTTCCGGCTACGTCAAATACCGAAAAC 11	Qy 220 GCTCGACGA
	Qy 256 CGCCCTTATCGAATCTGCCGAACAGCCTCGATTGCAATACTACATTTGGCGCAACGA 315
CAAAGACAAAGGCCTGACGGCAGCTCGTAACCAGCCTGCATGCCAAAACTTGTTG 12  [	Oy 316 CATTTCCGGCAGGCTGCTTCAACCTCATGTACCTTGCGGAGAACGCGGCGTGGCGCGT 375
TCATCGGCTCATCAACCTCGACCCCGGTTCGCAGGCTCA 13 TLAIGHT	Qy 376 ACGCCTGCTGCTTGGA
ATACCGAATGGGCTCGTCATCGAAAGCCCCAAAATCGCAGAACAGATGGAGCGCACCC 13 ATACCGAAATGGGGCTCGTCATCGAAAGCCCCAAAATCGCAGAACAGAACAGGAGGGCGCACCC 13	Qy         397 CAACACGCGCGTTGGA
TCGCCGATACCACACCGAATACGCCTACCG	Qy 415
	Qy 451 CGAAGTGCGCCTGTTCAACCCCTTCGTCCTACGCAAATGGCGCGCTCCGCTACCT 507
977 gGinLeuProHisGinGinValProArgLeuGinGinAlaProValArgArgLeuGinGl 997 1461 ATCCCGCCACAAAAACCTACCCGAACGAACGAAACGAAA	
	UD 232 FICALBLEULHISARGARGFROHISHISGIYPROFIC

Qy         1309	Db 605 GiyargGlyGlnArgGlnProAlaAlaAspAlaGluAlaAlaArgArg  Qy 1387 CACCCTGGCGATACCACCCGAATACGCCTACGGGT  Db (25 ArgProGlnGlnArgArgAlaArgSerGlySerProProCysSerPro  Qy 1426TACCCTGGCAAACAAACCAACCGCCC	5 C	TGS-11-096-568A-23618 US-11-096-568A Sequence 23618, Application US/11096568A Publication No. US20060048240A1 GENERAL INFORMATION: TAPLICANT: Alexandrov, Nickolai et al. TITLE OF INVENTION: Sequence-Determined DNA Fragments and (TITLE OF INVENTION: Therby	FOOKE	; FRATURE: ; NAME/KEY: misc_feature ; LOCATION: (1)(375) ; OTHER INFORMATION: Ceres Seq. ID no. 12414168 US-11-096-568A-23618	Alignment Scores: 3e-08 Length: 375 Score: 235.50 Matches: 119 Score Similarity: 35.2\$ Conservative: 46 Best Local Similarity: 25.4\$ Mismatches: 149 Query Match: 11 Gaps: 20	-10-665-	Oy 217 CCTGCTCGACGACGCCGTAGCGCTTGCCGGCCGCCGCCGTTAGCGAGCCCTTAGCGCGCCGCCGCCTTAGCGAGCCCTTAGCGCGCCGCCCTTAGCGCGCCGCCCTTAGCGAGCCCTTAGCGAGCG	Qy 337 CAACCTCATGTACCTTGCCGCAGAACGCGGCGTGCGCGTACGCTGCCTGC
556 CGCCGACAACCGCGCCACCATACTCGGCGACGCAATATCGGCGAATACTTCAAAGT 615 :::	GlnArgHisValArgGlyLeuArgAlaArgGlyHisArgAspValArgArgGlnArgPro	718 723	778ATACAACGACGAAACATCCAGACACGGGCTCCTGCGCTACCGCGAAAC 825 :::	886 CCAAACCCGCTGATCAGCGACACCCC	964 GCAAGACGCGCTCAAACAGCCCGAAAAAAGGTCTATCTGGTTTCACCCTATTTCGTCCC 1023		1144 CCGARANACCGIGCIGANGCGCAICANTEIREANNACCGIGCAIGNACCGAICANTEIREANNACCGIGCAIGNACCGAIGNACCAIGNACCAIGNACCAIGNACCAIGNACCAIGNACCAIGNACCAIGNACCAIGCGAIGCG		525 Aspargalyasparghiskrodiualahisvalvalhishenhisargalyalalala 544 1306 CCT 1308 
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ò	1309CGACCC 1314
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QQ	   S85 LeuGlnArgGluGlyAlaAspGlnArgHisArgProArgGlyArgValHisValArgGly 604
δλ	1342 GGGCGTCGTCAAAGCCCCAAAATCGCAGAACAGATGGAGCG 1386
a a	605 GlyArgGlyGlnArgGlnProAlaAlaAspAlaGluAlaArgArgArgAlaGlyGlyPro 624
ò	1387 CACCCTCGCCGATACCACACCCGAATACGCCTACCGCGT
qa	625 ArgProGlnGlnArgArgAlaArgSerGlySerProProCysSerProArgSerProGly 644
ò	1426TACCCTCGACAACAAACGCCTGCAATGGCACGA 1461
qq	645 SerArgArgSerSerAlaArgCysCysProArgArgTrpArgProProAlaTrpArgArg 664
ò	1462 TCCCGCCACCCGAAAAACTACCCGAAGA 1491
qq	665 ArgGlyHisArgProArgGlyGluProAspArg 675
RESULT US-11-( ; Seque ; Publi	RESULT 29 US-11-096-568A-23618 ; Sequence 23618, Application US/11096568A ; Publication No. US20060048240A1
AP	THILE OF INVENTION: Alector, Nickolai et al. TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Therby
	FILE REFERENCE: 2750-1592PÚS2 CURRENT APPLICATION NUMBER: US/11/096,568A CURRENT FILING DATE: 2005-04-01
S	NUMBER OF SEQ ID NOS: 34471 EQ ID NO 23618 LENGTH: 375
	TYPE: PRT OORANISM: Zea mays subsp. mays
•	FARJORY: misc_feature LOCATION: (1)(375) OTHER WHORMATION: Ceres Seq. ID no. 12414168
US-11	-11-096-568A-23618
Alignment Pred. No. Score:	Scores: 3e-08 Length: 235-50 Matches:
Perce Best Query DB:	t Similarity: 35.2% Conservative: 46 coal Similarity: 25.4% Mismatches: 14 Match: 15.4% Indels: 15.4% Indels: 15.4% Indels: 10.4%
US-10	-665-990A-13 (1-156
<i>δ</i>	157 CCTGGACAACATCCTGCAATCCGGCACACCCCTCATAACAACGGGCTATCGGACATCTA 216
qq	4 ProalaargargGlnHisSerProThrHisGlyValargSerArg 18
ò	217 CCTGCTCGACGACCCCACGAAGCCCTTGCCGCGCCGCCCCTTATCGAATCTGCCGA 276
qa	19 AlaAlaGlyArgArgGlyArgValProGlyArgAlaValArg 32
ò	7 ACACAGCCTCGATTTGCAATACTACATTTGGCGCAACGACATTTCCGGCAGGCTGCTGTT
g	33 ValGinArgArg 36
ò	337 CAACCTCATGTACCTTGCCGCGAGAACGCGGCGTGCGCGTACGCCTGCTGTTGGACGACAA 396
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Sequence 19864, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE: 2750-1592P025

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PELICATION NUMBER: US/11/096,568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 19664
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638 ValThrSerAlaProAspThrArgProAlaProGlySerThrAlaProProAlaHisGly 657
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                                                     1482 ACCCGAACGAACCCG-----AAGCCAAACTTTGGAAACGCATCGCCG 1523
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Matches:
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NAME/KEY: misc_feature
LOCATION: (1)...(766)
SOTHER INFORMATION: Ceres Seq. ID
US-11-096-568A-19864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1026 CAAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGACGGCATAGACGTTACCGTCC 1085
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|ProGlySer-----ThrAlaProProAlaHisGlyValThrSerAlaProAsp 363
                                                                                                                                                                                                                                                                                                                                                                                                                                          ACGCGCTCCTGC-----GCTACCGCGAAACCGTCGAAC-----AGTCGCCCCTCT 845
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                    GCGCCACCATACTCGGCGGACGCAATATCGGCGACGAATACTTCAAAGTCGGTGAGGACA 626
                                                                                                                                            CCGTTTTCGCCCACCTGGACATCCTCGCCACCGGCAGCGTCGTCGCCGAAGTATCGCACG 686
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|------AlaHisGlyValThrSerAlaProAspThrArgProAla
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 TGACCGACTTCCCCCCGCCTCAACCGCCGCATGCAAAAAATCCTTTACCGCCGACAACC
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qq	592 ProLeuglinArgGluGlyAlaAspGlnArgHisArgProArgGlyArgValHisValArg 611
λō	1417 CTACCGCGTTACCCTCGACAACAACAACGCCTGCAATGGCACGATCCCGCCACCCGAAA 1476
qq	612 GlyGlyArgGlyGlnArgGlnProAlaAlaAspAlaGluAlaAlaArgArgAlaGlyGly 631
ò	1477 AACCTACCGGAAGGAACCGGAAGCCAAACTTTGGAAAGGCATGGC 1521
Dp	632 ProArgProGlnGlnArgArgGlyAlaGlyAlaLeuHisValLeuGlnAspHisGln 651
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qq	652 ValArgGlyGlyAlaPro 657
RESULT	T 32 - 1964-5688-28958
Seq ;	; Sequence 28958, Application US/11096568A ; Publication No. US20060048240A1
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r.	TLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide- TLE OF INVENTION: Therby
F.	LE REFERENCE: 2750-1592PUS2 RRENT APPLICATION NUMBER: US/11/096,568A
E S	CURRENT FILING DATE: 2005-04-01 NUMBER OF SEQ ID NOS: 34471
20	EQ ID NO 28958 LENGTH: 1480 TYDE: DR
	iifn: Fri FERTURE: Arabidopsis thaliana
	NAME/KEY: misc_feature LOCATION: (1): (1480) OTHED INFORMATION: CAPES GOT ID NO 2006.666
us-11	ed: 10: 303266
Alignment Pred. No.:	ent Scores: 5.7e-08 Length:
Percen Best L Query	t Similarity: 32.5% Macches: 1 constructs: 32.5% Conservative: 4 coal Similarity: 25.3% Mismatches: 2 Match: Indels: 1
DB:	11 Gaps:
US-10-665	-665-990A-13 (1-1561) x US-11-096-568A-28958 (1-1480)
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ò	94 ATGGTTGCCCCCACTGGAAGAACGAAGGCGGTCATTTCAATACTTCCAAACCTGT 153
qq	113 ProProHisProLysProArgProHisProLysProProAsnVal 127
ò	154 CCTCCTGGACAACATCCTGCAAATCCGGCACACCCCTCATAACAACGGGCTATC 207
අු	128 LysProHisProHisProLysProProThrLysProHisProHisProLysProProThr 147
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ò	237 AAGCCCTTGCCGCCCGCGCCCCTTATCGAATCTGCCGAACACAGCCTCGATT 290
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1431 TCGACA-----AACACAACCGCC 1448
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506 AlalleProProValAlaLysProProValValThrProProThrAlaThrProProlle 525
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Sequence 1000, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT KIMMERIX' WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 1000
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                                                           TCTTCATCGGCTCATTCAACCTCGACCCCCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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LOCATION: (442)
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                                   ---SerThrProGlnProProThrHisLysProProProCysThrProThr----- 199
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243 ThrIleProProValAlaThrProProlleThrThrProProlleAlaAsnProProlle 262
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263 IleMetProProlleAlaThrProProValAlaAlaProProlleThrAsnProProlle 282
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---ProProValAlaSerProProMetAla------ThrProProThrGln-----
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------HisArgProGlnPheLysPheAspGln 297
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GAAGTGCGCCTGTTCAACCCCTTCGTCCTACGCAAATGGCGCGCACTCGGCTACCTGACC
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251 AspTyrLeuGlyLeuGlyLysLeuGlyTyrTrpArgAspThrHisThrArgValGlnGly
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Sequence 487, Application US/11050857
Publication No. US20060040278A1
GENERAL INFORMATION:
APPLICANT: COMPUGEN Ltd
TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, ITLE OF INVENTION: THEREOF FOR DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 1847.1005
CURRENT APPLICATION NUMBER: US/11/050,857
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 1150
SEQ ID NO 487
LENGTH: 1255
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Matches:
Conservative:
Mismatches:
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FILE REFERENCE: 1847.1003
CURRENT APPLICATION NUMBER: US/11/043,806
CURRENT FILING DATE: 2005-01-27
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 398
LENGTH: 1255
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Publication No. US20060051774A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel Nucleotide and Amino Acid Sequences, and Assays and Methods
TITLE OF INVENTION: thereof for Diagnosis of Prostate Cancer
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| ThrArg-------ProAlaProGlySerThrAlaProProAlaHisGlyVal 738
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aProProAlaHisGlyValThrSerAlaProAsp 7 (CAAACCGTCGAACAGTCGCCCTCT 8	757 1026 767 1086 781 1140 801	Db 821 AlaProAspThrArgProAlaProGlySerThrAjaProProAjaHisGlyVal 838  Qy 1236	Qy 1440 ACAACCGCCTGCAATGGCACGATCCCGCCACCCGAAAAACCT 1481

11 Gaps: 20 10-665-990A-13 (1-1561) x US-11-096-568A-20771 (1-413)	154 CCTCCTGGACAACATCCTGCAAATCCGGCACACCCCTCA 16	CTACCTGCTCGACGACCCCCACGAGGCCCTTGCCGCCCGCGCCGCCCTTAT	34AlaArgGluAsnProHisSerProIleProThrProGlnProProPheFroPro 51 265 CGAATCTGCCGAACACAG	ArgLeuLeuGln1leGlnSerSerProSerAlaAsnProProArgLeuGln1le		364CGGCGTGCGCGTACGCCTGCTGTTGGACGACAACACGGGCGG 408	409 GTTGGACGATCT	436CAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCTACGCAA 486        ::	ATGGCGCGCACTCGGCTACCTGACCGACTTCCCCCGCCTCAACCGCCGCATGCACAAA 54		161ProAlaSerProProThrGlySerProCysSerSerSerBroProThrSerSer 180	607 CTTCAAAGTCGGTGAGGACA	652 CGCCACCGGCACGTCGTCGCGAAGTATCGCACGACGTCGACCGCTACTG 702	200 hrProProSerAlaThrArgSerProSerArgAlaCysSerProSerCysProAlaSerG 220 703 GGCAAGCGATTCCG		730 GCGCATCATCCGCAGCGGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAA 783 .::       ::::     :::	CGACGAAACATCGAGACACGCGTCCTGCGCGAAACGGTCGAACAGTCGCC 8		841 CCTCTACCAAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTGAT 900		901 CAGCGACACCCCTGCAAAAGGACTCGACCGGCGGGGAAACCGCCGATTGCCGGGAG 960 		305 SerSerGlyGlySerSerSerProArgValLeuSerSerSerArgSerThrSerSer 324	1021 CCCTACAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGACGGCATAGACGTTAC 1080
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1110 ACGTTGCCGCCGTCCATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCA 1169
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-35
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3385
LENGTH: 715
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TITLE OF INVENTION: Novel full length CDNA
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WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
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OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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IRIE, RYOTARO
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CORGANISM: Homo sapiens
US-11-072-512-3385
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Search completed: May 2, 2006, 06:05:44 Job time: 124.5 secs

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acinetobact

burkholder

rhizobium l

pseudomonas rhizobium m

vibrio

burkholderi photobacter

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STRAIN-1291;
MEDLINE=22935225; PubMed=14573659;
DOI=10.1128/AIA.7.1.11.6381-6391.2003;
Bedwards J.L., Entz D.D., Apicolla M.A.;
"Gonococcal phospholipase d modulates the expression and function of complement receptor 3 in primary cervical epithelial cells.";
Infect. Immun. 71:6381-6391(2003).
EMBL; AY307929; AAG77221.1 -; Genomic DNA.
GO; GO:0003824; F:catalytic activity; TEA.
GO; GO:0003152; P:metabolism; IEA.
InterPro; IPR001735; PLD.
SMART; SM00155; PLDc; 2.
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Name=pld;
Neisseria gonorrhoeae.
Bacteria, Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Matches:
Conservative:
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Gaps:
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              041R64_9BURK
08041_VIBPA
080641_VIBVU
080661_VIBVU
080860_VIBVY
04FTL4_9GAMM
08FIM4_XANAC
08NUT_BDEBA
08FUM7_XANCP
080V8 IDILO
04UW7_XANCP
086UBS_BARNE
089NZ3_RHILO
080ES3_ACRTS
0984B3_RHILO
065B83_ACRTS
0984B3_RHILO
065B83_ACRTS
0984B3_ACRTS
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0984B3_ACRTS
066B3_ACRTS
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088BC2 PSESM
063J33 BURPS
061J13 PHOPR
04ZZX0 PSESY
05E616 V1BF1
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PROSITE; PSS0035; PLD; 2.
NON TER 525 525
SEQÜENCE 525 AA; 59224 MW;
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Q6W764;
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Q5ft87 neisseria g
Q9jtt1 neisseria m
Q9jyu0 neisseria m
Q7vuj6 bordetella
Q7w63 bordetella
Q8fi56 escherichia
Q8fi56 escherichia
Q8fi56 escherichia
Q87u5 shigella fl
Q7afa escherichia
Q57q10 escherichia
Q9ckm5 pasteurella
Q8x917 escherichia
Q9ckm5 pasteurella
Q82q98 salmonella
Q827m0 salmonella
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2898.236 Million cell updates/sec
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                                                                                                                                                           US-10-665-990A-13
2852
1 caaaatacaggcaatgccgt......tgcccatcgaaggtttatta 1561
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Biocceleration Ltd.
                                                                                                  May 2, 2006, 05:02:04 ; Search time 76 Seconds
                                                                      protein search, using frame_plus_n2p model
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Q5F887_NEIGI
Q9JTTI_NEIMA
Q9JYUQ_NEIMB
Q7VUJ6_BORPE
Q7WB63_BORPE
Q8FIS6_ECOL6
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Q57QL0 SALCH
Q8X917 ECO57
Q9CKM5 PASMU
Q8ZQ28 SALTY
Q8Z7M0 SALTI
Q5PGY9 SALPA
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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1: uniprot_sprot:*
2: uniprot_trembl:*
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Lewis L.A., Gillaspy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,

Nombey T., Hartman K., Nydick C., Carson M.S., Vaughn J., Thomson C.,

Song L., Lin S., Yuan X., Najar F., Zhan M., Ren Q., Zhu H., Qi S.,

A. Renton S.M., Lahi H., White J.D., Clifton S., Roe B.A., Dyer D.W.;

The complete genome sequence of Neisseria genorrhoeae.";

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

IL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

R EMBL, AEGO4969; AAW89600.1; -; Genomic_DNA.

R Fam; PRO04961; PLDC; 2.

R RAART; SMO0155; PLDC; 2.

R RAART; SMO0155; PLDC; 2.

R ROSITE; PSS00335; PLD; 2.

R Complete proteome.

R Complete proteome.
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                                  GTCCCCGCCACAAAAGACAAAGGCCTGACCGGCAGCTCCGTAACCAGCCTGCATGCCAAA
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-May-2005 (TrEMBLrel. 30, Last annotation update)
NorderedLocusNames=NG0902;
NorderedLocusNames=NG09902;
NorderedLocusNames=NG00902;
NorderedLocusNam
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NEDLINE=2017575; PubMed=10710307; DOI=10.1126/Science.287.5459.1809;
Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
Hickey B.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
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Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
Venter J.C.;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cardiolipin synthetase family protein.
OrderedLocusNames=NNB1434;
Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
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EMBL; AE002098; AAF41795.1;
PIR; B81083; B81083.
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KW         Complete protecome.           SQ         SEQUENCE         508 AA;         57350 MW;         A2DE6CAC47CA25D5 CRC64;           Alignment         Scores:         1.89e-135         Length:         508           Pred. No.:         2573.00         Matches:         497           Score:         88*         Conservative:         5           Best Local Similarity:         97.8*         Mismatches:         6           Query Match:         2         Gaps:         0           DB:         2         Gaps:         0           US-10-665-990A-13 (1-1561) x Q9JYUO_NEIMB (1-508)         1-508)	Oy 38 AIGAAAACACGCAGCCTCATTTTATGCCTCCTTCTCTGTTCATGTTCTTCATGG 97	158 CTGGACAACATCCTGCAAATCCGGGACCCTCATAACAAGGGCTATCCGACATCTAC  [	CACAGCCTCGATTTGCAATACTACATTTGGCGCAACGACATTTCCGGCAGGCTGCTGTTC	398 398 121 124 458	CCATA       hrile rcgcc 	Qy         638 GACCTGGACATCCTGGCACCGGCAGCGTCGTCGGCGAACTATCGACCGC 697           Db         201 AspLeuAsp1leLeuAlaThrGlySerValValGlyGluValSerHisAspPheAspArg 220           Qy         698 TACTGGCCATTCGCCCAACCGCATCATCCGCAACAACATCGGC 757           Db         221 TyTTpAlaSerHisSerAlaHisAsAALAThrARGLIB[	AGGGTCTTCAAGCACTCGGATACAACGACGAAACATCCAGGACACGCGCTCCTGCGCTACTACTACAACGACAACGCGCGTCCTGCGCTACTACAACGACAACGCGCGCTCCTGCGCTACTACAACGACACGCGCTCCTGCGCTACTACAACGACCGCGCTCCTACCAACGAACCGTCGAACCGTCGAACCGTCGCCCCTCTACCAAAAATACAGACGGGACCATCGGTGGTAAAAATACAGACGGGAACCGTGGTAAAAAATACAGACGGGAACCGTGGTGGTAAAAAATACAGACGGCACCGCTGATCAGCGCACCCCTGATCAGCGAACCCCTGATCAGCGCACCCCTGATCAGCGCACCCCTGATCAGCGCACCCCTGATCAGCGACACCCCTGCAAACGACCCGCCGCCGCGCGCG

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    ----GCGCTCCTGCGCTACCGCGAAACCGTC
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Q1-OCT-2003 (TrEMBLE1. 25, Last sequence update)
Q1-MAR-2004 (TrEMBLE1. 26, Last annotation update)
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Nat. Genet. 35:32-40(2003).

BMBL: BX64040; CAR543560.1; -; Genomic DNA.

GO; GO:0003824; F:catalytic activity; TEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPRO01736; PLD.

Ffam; PF00614; PLDc; 2.

SMART; SM00155; PLDc; 2.

PROSITE; PSS0035; PLD; 2.
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                                                                      ACGCGCATCATCCGCAGCGCCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGAC
                                                                                                   GlyProLeuLeuProAla-------ProGlyAlaGinThrLeuArgAlaLeuAla
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RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungail K.L., Ra Cerdeno-Tarraga A.M., Temple L., James K.D., Harris B., Quail M.A., RA Cerdeno-Tarraga A.M., Temple L., James K.D., Harris B., Quail M.A., RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Gromparative analysis of the genome sequences of Bordetella pertussis, Nat. Genet. 39:32-40(2003).

RY GO, GO:0003824; F:catalytic activity; TEA.

ROG, GO:0008122; P:metabolism; IEA.

RY SMART; SM00155; PLDC; 2.

RY SMART; SM00155; PLDC; 2.

RY SCONDERCE 492 AA; 53309 MW; BCGBFEBBAC34E726 CRC64;
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Enterobacteriaceae, Escherichia.
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01-NOV-1997 (Rel. 35, Last sequence up
13-SEP-2005 (Rel. 48, Last annotation
Hypothetical protein ymdC.
NAMMe=ymdC; OrderedLocusNames=b1046;
Escherichia coli.
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                                                                                      MEDLINE=22386234; PubMed=12471157; DOI=10.1073/pnas.25529799;

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R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016621; C:integral to membrane; IEA.

GO; GO:0008654; P:phospholipid biosynthesis; IEA.
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            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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SEQUENCE 493 AA; 55876 MW; 582F673DC3BBDC7A CRC64;
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85
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                            CFT073 / ATCC 700928;
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Best Local Similarity:
Query Match:
DB:
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234 HisAsnAspAlaMetThrHis------ArgTyrLeuArgLysMetGluSerSer
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                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).

[L. Science 277:1453-1474(1997).

[L. Science 277:1453-1474(1997).

[L. SCIENCE SEQUENCE [LARGE SCALE GENOMIC DNA].

[L. NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

[L. STRAIN=FK12;

[L. MEDLINE=97061202; PubMed=8905232;

[L. MEDLINE=97061202; PubMed=8905232;

[L. MEDLINE=97061202; PubMed=8905232;

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[L. MEDLINE=97061202; PubMed=8905232;

[L. MEDLINE=97061202; PubMed=8905232;

[L. Memoto K., Inada T., Itoh T., Kajihara M., Kashimoto K., Kashimoto H., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., Miki T., 
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-K12 / MG1655,

MEDLINE-97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;

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REMBL; D90741; BAA35844.1; -; Genomic_DNA.

REMBL; D90742; BAA35844.1; -; Genomic_DNA.

RECHORASE; EB3634; -.

RECHORASE; EB3634; -.

RECHORASE; EB3634; -.

RECHORASE; EB3634; -.

RECHORASE; EB3634; -.

RECHORASE; RB01736; PLD.

RECHORASE; RB01736; PLD.

REMART; SN00155; PLDc; 2.

REMART; SN00155; PLDc; 2.

ROWNET; SN00155; PLD; 2.

ROWNET; ROWNET; RPCHOME; PLD; 2.

REMART; RN00155; PLD; 2.

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PLD phosphodiesterase 2.
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STRAIN=2457T / ATCC 700930 / Serotype 2a;
MEDLINE=225074; PubMed=12704152;
MEDLINE=225074; PubMed=12704152;
MEDLINE=225074; PubMed=12704152;
Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Mei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Mu B., Perra N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
Complete gancine sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T ";
Infect. Immun. 71:2775-2786(2003)
Infect. Immun. 71:2775-2786(2003)
EMBL; ABO16981; AAP16548.1; -; Genomic DNA.
EMBL; AGO16981; AAP16548.1; -; Genomic DNA.
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                                                                                                                        US SHIFL

QB3RU5_SHIFL
QB3RU5_SUCY89;
QB3RU5_QUUCY81
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QB1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
QB1-JUN-2003 (TrEMBLrel. 31, Last annotation update)
Putative synthase.
Name=ymdC; OrderedLocusNames=S1116, SF1042;
Banjeella flexneri.
Banjeella flexneri.
Bacteria; Protecobacteria; Gammaproteobacteria; Enterobacteriales;
Buterobacteriaceae; Shigella.
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STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHEC;

KN MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

H Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Tobe T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

LI DNA Res. 811-22(2001).

CO GO:0003824; F:catalytic activity; TEA.

RO; GO:000315; P:metabolism; IEA.

RINTEPPO: IPRO01736; PLD.

RR PFEME; SMO0155; PLDC; 2.
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470 GlubroAlaThrSerPheTrpLysArgValMetValArgLeuAlaSerIleLeuProVal 489
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=81334;
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Matches:
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SEQUENCE 493 AA; 55928 MW; DEC407F83D7D1CFF
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C7AFA8;
05-JUL-2004 (TERMELrel. 27, Cr
05-JUL-2004 (TERMELrel. 27, La
05-JUL-2004 (TERMELrel. 27, La
Dutative synthase-
orderedLocusNames-EC81424;
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             GAACCCGAAGCCTTTGGAAACGCATCGCCGCAAAAATCCTATCCCTGCTGCCCATC
                          -----CCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACGACCCCCCACGAAGCC
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STRAIN=SC-B67;

PubMed=15781495;

Chi C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,

Wang H.-S., Lee Y.-S.;

"The genome sequence of Salmonella enterica serovar Choleraesuis,

highly invasive and resistant zonocic pathogen.";

Nucleic Acids Res. 33:1690-1698 (2005).

EMBL; AE017220; AAX65001.1; -; Genomic_DNA.
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Q57QLO_SALCH PRELIMINARY; PRT; 528 AA.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Putative phospholipase.
Putative phospholipase.
Name=ymdC; OrderedLocusNames=SC1095;
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=591;
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-015:147 / EDL333 / ATCC 700927 / EHEC.

MUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

A BOSE D.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., A Grotbeck E.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., A Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., A Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., A Welch R.A., Blattner F.R.;

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"Mature 409:529-533(2001).

"Nature 409:529-533(2001).

"Nature 409:529-533(2001).

"R PIR, H90806; H90806.

"PRADI, ARGS5792.1; -; Genomic_DNA.

"PIR, H90806; H90806.

"R PIR, H90806; H90806.

"R PIR, H90806; H90806.

"Mature 409:529-533(2001).

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"Mature 409:529-533(2001).

"Mature 409:529-633(2001).

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Escherichia coli O157:H7.
Escherichia coli O157:H7.
Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Name.r.o. synthase.
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Matches:
Conservative:
Mismatches:
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TyrTrpAsnSerProSerSerTyrProLeuGluSerIleIleIleArgAspProlleThr 248
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TyrAlaPheSerValLysLeuAsnGluAlaGlnAlaLeuTyrTrpGluThrGlnGluAsn 482
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PheArgLeuAsnArgArgMetHisAsnLysSerPheThrAlaAspGlyValMetSerlle
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443 IleAspSerProGluLeuAlaArgLeuLeuSerAspGlyLeuGlnGlnAsnGlnAlaAsn
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17 LeuPheSerLeuVallleLeuAlaLeuIleSerTyrGlnArgLeu-----ProThrSer
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                                                                                                                                                                                                                                                                                                                                                                                              WUCLEOTIDE SEQUENCE.
STRAIN=PM70;
MEDLIN=PM70;
MEDLIN=2114586; PubMed=11248100; DOI=10.1073/pnas.051634598;
MAY B. J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
BMBL, AR006196; ARX03670.1; -; Genomic DNA.
GO; GO:0016740; F:transferase activity? IEA.
GO; GO:001874; PLDC: 2.
Pfam: PF00614; PLDC: 2.
                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Pasteurella.
NCBI_TaxID=747;
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C65B0EB65D80F216 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PM1586.
OrderedLocusNames=PM1586;
Pasteurella multocida.
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Matches:
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is PASMU
QGCKMS_PASMU PRELIMINARY;
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    GAAGGITIATIA
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                                                                           GCCGGGAGGCTGCAAGACGCGCTCAAACAGCCCCGAAAAAAGCGTCTATCTGGTTTCACCC
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     GACAACCGCGCCACCATACTCGGCGGACGCAATATCGGCGACGAATACTTCAAAGTCGGT
                   |||
| AspGlyValValThrLeuValGlyGlyArgAsnIleGlyAspAlaTyrPheGlyAlaGly
                                                           GAGGACACCGTTTTCGCCGACCTGGACATCCTCGCCACCGGCAGCGTCGTCGCCGAAGTA
                                                                                                                 680 TCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAACGCCACGCGCATCATC
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                                                                                                                                                                                                                                                         233 SerTrpTyrAsnAspGluIleThrArg------ArgTyrLeuHisLysLeuGlu
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249 ThrSerGlnPheMetAlaAspLeuAspArgGlyThrLeuProLeuIleTrpAlaLysThr
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|LeuAspArgTrpGlyArgIleAsnTrpIleAspArgGlnGlnGluGluGluLysValLeu
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Salmonella typhimurium.
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative phospholipase.
TrpCysLeuSerTrpLeuProValGluHisLeuLeu 514
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Nature 413:852-856(2001).
Rature 413:852-856(2001).
EMBL; AB2008749; AALZOOTS 1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00016740; F:transferase activity; IEA.
GO; GO:0008615; P:metabolism; IEA.
GO; GO:000865; P:phospholipid biosynthesis; IEP.
R InterPro; IPR001736; PLD.
R Pfam; PF00614; PLDc; 2.
R SWART; SW00155; PLDc; 2.
R PROSITE; PS50035; PLD; 2.
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GCAGAACAGATGGAGGGCACCCTCGCCGATACCACACCCGAATACGCCTACCGCGTTACC 1429
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|AlaThrLeulleHisLysArgPheThrGlnSerGlnArgAspAlaAlaTrpGlnLeuArg 449
                                                                                                                                                                       ThrserGlnPheMetAlaAspLeuAspArgGlyThrLeuProLeuIleTrpAlaLysThr
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STRAIN=TY2 / ATCC 700331;
MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                  MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., White N., Farrar J., Krogh A., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
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        OSCINGA SALTI PRELIMINARY; PRT; 495 AA.

OSCING, Q7CSA7;

O1-MAR-2002 (TrEMBLrel. 20, Created)

O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)

O1-MAR-2005 (TrEMBLrel. 29, Last annotation update)

Hypothetical protein STY1185.

OrderedLocusNames=STY1185, t1772;

Salmonella typhi.

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

Enterobacteriaceae; Salmonella.
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EMBL, AE018840; AA069395.1; -; Genomic_DNA.
EMBL, AE018840; AA069395.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
INTERPORT IPRO17136; PLD.
Pfam; PF00614; PLDC; 2.
SMART; SM00155; PLDC; 2.
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Matches:
Conservative:
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Complete proteome; Hypothetical
SEQUENCE 495 AA; 56348 MW; 4
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Whomed=15531882; DOI=10.1038/ng1470;

Rochelland M., Sanderson K.E., Clifton S.W., Latreille P.,

McClelland M., Sanderson K.E., Elifton S.W., Latreille P.,

McClelland M., Sanderson K.E., Bergin T., Ozersky P., McLellan M.,

Harkins C.R., Wang C., Nguyen C., Bergin E., Elliott G.,

Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,

Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,

Delehauuty K., Fronick C., Magrini V., Mian M., Warren W., Florea L.,

Spieth J., Wilson R.K.;

"Comparison of genome degradation in Paratyphi A and Typhi, human-
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                                                  CCGAACGAACCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATCCTATCCCTGCTG
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Salmonella paratyphi-a.
Salmonella paratyphi-a.
Salmonella paratyphi-a.
Enterela paratyphi-a.
Enterobacteriacede; Salmonella.
NCBI_TaxID=54388;
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SEQUENCE 495 AA; 56310 MW; 8BAADE58874983A2 CRC64;
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77
147
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein ymdC.
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Conservative:
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NUCLEOTIDE SEQUENCE.
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GlnSerLeuLysGlnGlnLeuAspAspTyrTyrGlnGluValThrValGlnAsnTyrLeu
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|Trp-----VallysAlaThrValValLysAspAlaProAspLysIleArgAlaLysAla
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TyrTrpAsnAspGluTyrAlaTyrSerValGlnAsnIleVal-------
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|HisGlyPro---GluValThrGlnTyrAlaTyrAspIleAspThrSerGlnThrSerLeu
                      CCGAACGAACCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATCCTATCCCTGCTG
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Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,

Labarret L., Cruveiller S., Robert C., Duprat S., Wincker P.,

Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;

"Unique features revealed by the genome sequence of Acinetobacter sp.

ADP1, a versatile and naturally transformation competent bacterium.";

Nucleic Acids Res. 32:576-5779(2004).

GO: GO: 0016740; F: transferase activity; IEA.

GO: GO: 0016740; F: transferase activity; IEA.

FIRED: PRO01736; PLD.

PF00614; PLDC: 2.
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Moraxellaceae, Acinetobacter.
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Putative phospholipase D protein.
OrderedLocusNames=ACIAD3001;
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ThrLeuSerLysPheIlePheAlaSerMetPheSer--
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ThrAspProAlaGlySerGlyArgLeuLySTrpValGlnThrAspAlaAspGlyLysVal
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||| ThrGluIleAspHisGluProGluValSerAlaProArgArgMetGluValTrpPheLeu
  CATGCCGTCCCCGCCACAAAGACAAAGGCCTGACCGGCAGCTCCGTAACCAGCCTGCAT
                       GlyAspLysSerIleSerLys---GlnValIleIleGlySerArgAlaSerLeuHis
                                                                              GCCAAAACCTTCATTGTGGACGCAAACGCATCTTCATCGGCTCATTCAACCTCGACCCC
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STRAIN=RIND 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12650739; DOI=10.1016/S0140-6736(03)12659-1;
MAKINO K., OSHIMB K., KUTCKAWA K., YOKOYAMA K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasuunaga T., Shinagawa H., Hattori M., Iida T.;
Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
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01-JUN-2003 (TYEMBLrel. 24, Last sequence update)
01-JUN-2004 (TYEMBLrel. 26, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
01-JUN-2004 (TYEMBLrel. 26, Last annotation update)
02-Zeardal protein VRA0341;
03-Zeardal protein VARION (Sammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
03-Zeardal Vibrio.
04-Zeardal Vibrio.
05-Zeardal Vibrio.
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EMBL; BA000032; BAC61664.1; -; Genomic DNA.
GO; GO:000324; F:catalytic activity; TEA.
InterPro; IPR001735; P:metabolism; IEA.
PF001736; PLD.
PFam; PF00614; PLDC; 2.
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        CGCAGCCTCATTTCCCTTTTATGCCTCCTTCTTCTTCATGTTCTTCATGGTTGCCCCCA 106
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Phosphatidylserine/phosphatidylglycerophosphate/ cardiolipin
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Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of Vibrio vulnificus CWCP6."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AE016810; AA007638.1; -; Genomic_DNA. GO; GO:0016410; F:transferase activity; IEA. GO; GO:0008152; P:metabolism; IEA. InterPro; IPR001736; PLD. Pfam; PF00614; PLDC; 2. SWART; SMOMISS; PLDC; 2.
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Vibrio vulnificus.
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TyrAspSerGluProGluSerSerIleTrpArgSerIleGlyAlaTrpLeuSerGlyVal 494
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GTCCATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTAC
        CCCAAAATCGCAGAACAGATGGAGCGCACCCTCGCCGATACCACCCCGAATACGCCTAC
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Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Phopholipase D-family protein.
OrderedLocusNames=VV13126,
OrderedLocusNames=VV3126,
Vibrio vulnificus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Vibrio vulnificus CMCP6."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AE016807; AA0114471,; ; Genomic DNA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:001674; P:metabolism; IEA. InterPro; IRRO1736; PiD. Pfam; PF00614; PiDc; 2. SNART; SM00155; PiDc; 2.
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|TrpTyrTrpGlyLysGlyGlnValTrpTyrAspLeuProAspLys------ValAsp 318
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140 ACTICCAAACCIGICCICCIG-----GACAACAICCIGCAA-----AICCGG
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|HisHisProGlnAspArgGluAsnLeuThrAlaPhePheProLeuAspLysGlyHisAsp
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US-10-665-990A-13 (1-1561) x Q7MMB3_VIBVY (1-554)	OY 29 ATATCCCGATGAAAACACGCAGCCTCATTTCCCTTTTATGCCTCCTTCTC 79		125AGCCGTCATTTCAATACTTCCAAACCTGTCCTCGTG	GCTATCCGACATCTACCTG 2    ::: nLeuThrAlaPhePhePro 1	Qy 221 CTGACGACCCCACGAAGCCTTGCCGCGCGCCGCCCCTTATCGAATCTGCGAACAC 280		Qy 341 CTCATGTACCTTGCCGCAGAACGCGGCGTGCGGTACGCCTGCTGTTGGACGACAACAAC 400 ::::::	Qy 401 ACGCGCGGTTGGACGATCTCCTGCTCGACGACGCCATCCCCAATATCGAAGTGCGC 460	Qy 461 CTGTTCAACCCCTTCGTCCTACGCAAATGGCGCACTCGGCTACCTGACCGACC	Qy 521 CGCCTCAACCGCCGCAACAAATCCTTTACCGCCGAAACCGCGCCACCATACTC 580	Qy 581 GGCGGACGAATATCGGCGACGAATACTTCAAAGTCGGTGAGGACACCGTTTTCGCCGAC 640	Oy 641 CTGGACATCCTCGCCACCGCAGCGTCGTCGGCGAAGTATCGCACGACTTCGACCGCTAC 700	701 TGGGCAAGCCATTCCGCC	Oy 740 CGCAGCGCAACATCGGCAAGGTCTTCAAGCACTCGGATACAACGAACATCC 796 ::         Db 293 GluGluGluLeuGlnAlaTrpLeuLysGluThrGlnLeu 305	Qy 797 AGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGCGCCCCTCTACCAAAAATA 856 :::	Qy 857 CAGACGGGACGCATCGACGGCGCCCGAAACCCGGCTGATCAGCGACCCCTGCA 916	Qy 917 AAAGGACTCGACCGCGACGCCGAAACCGCCGATTGCCGGGAGGTGCAAGACGCGCTC 976	Qy 977 AAACAGCCGGAAAAAGGTCTATCTGGTTTCACCCTATTTCGTCCCTACAAAATCCGGC 1036 ::
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Choy H.E.;

"Complete genome sequence of Vibrio vulnificus CMCP6.";

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

E MBL, AB016807; AA011511.1; -; Genomic_DNA.

R GOS, GO:0008152; P:mtransferase activity; IEA.

R GO; GO:0008152; P:mtransferase activity; IEA.

R DITETPRO; IPR001736; PLD.

R Pfam; PF00614; PLDC; 2.

R SMART; SW00155; PLDC; 2.

R PROSITE; PS50035; PLD; 2.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
hopholipase D-family protein.
OrderedLocusNames=VV13197;
Vibrio vulnificus.
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NUCLEOTIDE SEQUENCE
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Query Match: 29.9% Indels: 39 DB: 2 Gaps: 7	Q4FTL4_9GAMM (1-570) ATGCCTCCTTCTCTGTTCATGTTCT		49 rGlnSerAspleSerLysGlnAspAsnlleGluLysAspValGlnLysAspGlnAspSe	Qy 164198 198 198 198 169 x1leaspThrThrLysaspThrThrAsnValSerThrAspThrValThrProAsnThrAs 89	QY 199 CGGGCTATCCGACATCTACCTGCTCGACGACCCCCCAGAA 238	Db 89 pSerLeuAspLeuValAlaAla1leSerGlnGlnSerLysIleHisProAspLeuSerGl 109 Qy 239	:::   :::     109 yTyrHisProlleValThrGlyAlaAsnAlaPheAlaSerArgSer1leLeuThrGlyMe 271 TGCCGAACAGGCTCGATTGCBATTACTAGATTTGGGGAGAGAGAGAGAGAGAGAGAGAGAG	129	331 GCTGTTCAACCTCATGCCGCAGAACGCGGCGTACGCGTACGCTGCTGTTGGA	Db 149 uMetLeuLysAspLeuTrpAspAlaAlaGluArgGlyValIleValArgLeuLeuLeuLa 169 Qy 391 CGACAACAACACGCGCGGGTTGGACGATCTCCTGCTCGCCTCGACACACCATCCAA 447		Qy 448 TATCGAAGTGCGCCTGTTCAACCCTTCGTCCTAAGTGGCGCGCACTCGGCTACCT 507		Qy 508 GACCGACTTCCCCGCCTCAACCGCCGCATGCAAATCCTTACCGCCGACAACCG 567	Qy 568 CGCCACCATACTCGGCGACGCAATATCGGCGACGAATACTTCAAAGTCGGTGAGGACAC 627	628 CGTTTTCGCCGACCTGGCCTCGCCACGGCAGGTCGTCGCGAAGTATCGCACGA	249 rGlnPheAlaAspLeuAspValLeuLeuIleGlyLysValValAlaAspIleAspAsnSe	Ay 688 CTCGACGCTACTGGGCAAGCCATTCGGCCACGCGCACGCGCATCATC 739	740CGCAGCGGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGAAAC	Db 289 pLysGlyGluThrThrAspPheValLysGlyLeuAspLysLeuLysThrAspGluLysSe 309	Qy 793 ATCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGTCGCCCTCTACCA 849	Db 309 rSerSerAsnGlySerLeuSerIleTyrLysalaalalleGluAspSerSerIleAspTh 329	850 AAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTGATCAGCGACAC :::	329 rAspLeulleAsnLysArgValProPheArgTrpThrAspMetGlnPheLeuSerAspAs		Db 349 pValGlyiysieuThrLysThrValProAlaAspThrAsnLeuValHisGlnLeuArgTh 369
	Qy     1085     CTGACCAACTCGCTACAGGCGACCGACGGTTGCCGCCTACCGGCTACGTCAATAC     1144       Db     346     ValThrAshSerLeualaSerAshAspValPheAlaValHisGlyTrpTyrAlaLysTyr     365	Oy 1145 CGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCAACCATGCCGTC 1204	1205 CCCGCCACAAAAGACATGACCGGCAGCTCCGTAACCAGCCTGCATGCCAAAACCC	LysArgGinTrpSerLeuileGlySerGlnArgAlaSerLeuHisAla 3TGGACGCAAACGCATCTTCATCGGCTCATTCAACCTCGACCCCGT	404	Oy 1325 CGGCTCAATACCGAAATGGGCGTCGTCATCGAAAGCCCCAAAATCGCAGAACAGATGGAG 1384 :::	Oy 1385 CGCACCCTCGCCGATACCACACCCGAATACGCCTACCGCGTTACCCTCGACAAACACAAC 1444	1445 CGCTGCAATGGCACGACCCGAAAAACTACCGAACGAAGCCAAA	Db 464		RESULT 24 O4 FTT-4 9GANM		13-SEP-2005 (TrEMBLrel. 31, Creat 13-SEP-2005 (TrEMBLrel. 31, Last	DT 13-SEP-2005 (TEMBLE) 31, Last annotation update) DE Probable phospholipase D. GN ORFNames-Psyc_0791;	US PSYCHIODACTER ATCITCUM 2/3-4. OC Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, OC Moraxellaceae, Psychrobacter. OX NCBI TaxID=259536;			Klappenbac Tiedje J.N	RT "Complete sequence of Psychrobacter arcticum 273-4."; Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.	NUCLEOT STRAIN=		Land M., Larimer F., Pitluck S., Richardson P., Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.	DR EMBL; CP000082; AAZ18644.1; -; Genomic_DNA. SQ SEQUENCE 570 AA; 63466 MW; 0ECC7DAĀ9ECA3BC1 CRC64;	Scores:	2.27e-39 Length: 852.00 Matches:	Conservative: Mismatches:

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176 ATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACGACCCCCAC 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P.; Tores S.M., White F.F., Setubal J.C., Kitajima J.P.; Tores S.M., White F.F., Setubal J.C., Kitajima J.P.; Ewo Xanthomonas pathogens with differing host specificities."; Mature 417:495-463(2002).

EMBL: AE011929; AMM37716.1; -; Genomic DNA.

GO: GO: 0003824; F: Catalytic activity; ĪEA.

GO: GO: 0003825; P: Retabolism; IEA.

InterPro; IPR001136; PLDC: 2.

Pfam; PR00114; PLDC: 2.
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IleAlaLeuLeuValLeuValLeuAlaSerAlaLeuSerLeuTyrGlyTyrGlyArgPhe
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-------ThrAlaValAlaThrProlleABpLysValValAlaProLeuGln
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850.50
52.7*
37.9*
29.8*
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Best Local Similarity:
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Pred. No.:
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STRAIN=306 / ATCC 13902 / XV 101;
STRAIN=306 / ATCC 13902 / XV 101;
STRAIN=306 / ATCC 13902 / XV 101;
STRAIN=306 / ATCC 13902 / XV 101;
STRAIN=306 / ATCC 13902 / XV 101;
A silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Auneida N.E., Camarot G.B., Van Sluys M.A.,
Almeida N.F. J.T., Alves L.M.C., do Amaral A.M. Bertolini M.C.,
Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F.,
Capina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
El-Dorry H., Farial J.B., Ferreira R.J.C.,
El-Dorry H., Fraina J.B., Ferreira R.J.C., Gruber A.,
El-Dorry M. I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
Locall E.C., Machado M.J., Madeira A.M.B.N., Martinac-Rossi N.M.,
Martins E.C., Machanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
                                                                                                                                                                                                                                                                                                                          449
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rAsnSerPheAspAlaThrAspValThrAlaValHisSerGlyTyrSerGlnTrpArgPr
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         CGCGCTCAAACAGCCCCGAAAAAAGCGTCTATCTCGTTTCACCCTATTTCGTCCCTACAAA
                                   rLeuLeuGlySerProSerLysLysLeuThrIleIleSerSerTyrPheValProThrLy
                                                                                                 ATCCGCCACAGACCCCACTGCCAAAACTGGTGCAGGACGCCATAGACGTTACCGTCCTGAC
                                                                                                                           ACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCAACCATGCCGTCCCCGC
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Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
NCBL_TaxID=92829;
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QBPIM4; XANAC PRELIMINARY;

QBPIM4;

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01-MAR-2004 (TrEMBLrel. 26, La

Cardiolipin synthase.
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                                                                             NUCLEOTIDE SEQUENCE.

STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;

Nubmed=4752164; DOI=40.1126/science.1093027;

Rubmed=1752164; DOI=40.1126/science.1093027;

A Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C., A Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F., Sockett R.E., Schuster S.C.;

A Sockett R.E., Schuster S.C.;

I A predator unmasked life cycle of Bdellovibrio bacteriovorus from condition perspective.;

Science 303:689-692(2004).

REMBL; BX842647; CAST78430.1; -; Genomic_DNA.

GO; GO:0003824; F:catalytic activity; IEA.

R GO; GO:0003824; F:catalytic activity; IEA.

R InterPro; IPR001736; PLD.

R FRMSTFS; SM00155; PLDC; 2.

R RART; SM00155; PLDC; 2.
            Bdellovibrio bacteriovorus.
Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
Bdellovibrionaceae; Bdellovibrio.
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Matches:
Conservative:
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                                                        NCBI_TaxID=959;
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06MQL7:
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative phospholipase D precursor.
          AGCCATTCCGCCCACACGCCACGCGCATCATCCGCAGC
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                                                                                         [1]—WUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=L2-TR / DSM 15497 / ATCC BAA-735;
STRAIN=L2-TR / DSM 15497 / ATCC BAA-735;
Pubmed=1559672; DOI=10.1073/pnas.0407638102;
Hou S., Saw J.H., Lee K.S., Freitas T.A., Belisle C., Kawarabayasi Y. Donachie S.P., Pikina A., Galperin M.Y., Koonin E.V., Makarova K.S., Omelchenko M.V., Sorokin A., Wolf Y.I., Li Q.X., Keum Y.S., Campbell S., Denery J., Aizawa S.-I., Shibata S., Malahoff A.,
                                                                                                                                                                                                                "Genome sequence of the deep-sea gamma-proteobacterium Idiomarina loihiensis reveals amino acid fermentation as a source of carbon a
                                                   Gammaproteobacteria; Alteromonadales;
                                                                                                                                                                                                                                                                                                                                                                             464 AA; 53557 MW; 59A8BFA13DEB45F7 CRC64;
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1186
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EMBL, AE017340; AAV82284.1; -; Genomic DNA.

GO; GO:0003824; F:catalytic activity; IEA.

InterPro. IPR001736; PLD.

SMART; SM00155; PLDc; 2.

PROSITE; PS50035; PLD; 2.
01-FEB-2005 (TrEMBLrel. 29, Last annotation update) Phospholipase D family protein.
OrderedLocusNames=IL1444;
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Matches:
Conservative:
Mismatches:
Indels:
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56.6%
40.2%
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Idiomarinaceae, Idiomarina.
NCBI_TaxID=135577;
                                        Idiomarina loihiensis.
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SEQUENCE 464 AA
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|ProThrArgAlaArgGluGlyThrLeuMetArgGlyValGluMetValLeuArgMetPhe
                                                                                                                  STRAIN-8004;
Olian W. Jia Y.-T., Ren S.-X., He Y.-Q., Feng J.-X., Lu L.-F.,
Sun Q.-H., Ying G., Tang D.-J., Wu W., Wang L.-F., Jiang B.-L.,
Zeng S.-Y., Gu W.-Y., Lu G., Rong L., Tlan Y.-C., Yao Z.-J., Fu G.,
Chen B.-S., Fang R.-X., Qiang B.-Q., Chen Z., Zhao G.-P., Tang J.-L.,
He C.-Z.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; CP000050; AAY48476.1; -; Genomic_DNA.
SEQUENCE 520 AA; 57165 MW; 8849CFED240410A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCAAATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACGAC
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Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=314565;
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                      -------IleTrpLysGlyTyr
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|LeuArgLysAspValArgProTyrPheArgArgSerAlaSerSerLeuHisAlaLysThr
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424 LysLeuTyrTrpLeuAspLysSerLysIleProAlaLeuArg-----LeuTyrLysGlu
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update,
13-SEP-2005 (TrEMBLrel. 31, Last annotation update,
Cardiolipin synthase.
ORFNames=XC_1408;
Xanthomonas campestris pv. campestris str. 8004.
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|SerSerAspLysProArgLeuPheAsnAsp
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ID QGUWUTY XANCP PRELIMINARY;

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R. Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
R. Setubal J.C., Kitajima J.P.; Genomic DNA.
B. Setubal J.C., Kitajima J.P.; Genomic DNA.
B. R. Mella AROll338; Apall978; P.J.; Genomic DNA.
GO; GO:0003824; F.catalyvic activity; IEA.
B. ROSSINE, PRESOUSS; PLDC; 2.
B. RART; SM00155; PLDC; 2.
B. RRORITS; PSS0055; PLD; 2.
B. RRORITS; PSS0055; PLD; 2.
B. R. ROSSINE; PSS0055; PLD; 2.
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|ArgAlaMetAsnLeuAsnThrGluMetGlyLeuLeuPheGluAspArgThrValThrAla
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MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Monterior-Vitorello C.B., Van Sluys M.A.,
Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xanthomonas campestris (pv. campestris).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
Xanthomonadaceae, Xanthomonas.
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QBP7A5;
01-OCT-2002 (TrEMBLrel. 22, Ls
01-OCT-2002 (TrEMBLrel. 22, Ls
01-MRA-2004 (TrEMBLrel. 26, Ls
Cardiolipin synthase.
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LeuAspSerGlnLeu
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Q8P7A5 X
Q8P7A5 X
Q8P AC Q8P
DD O1-
DD O1-
DD O1-
DD O1-
DD CAR
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                          GGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAACA
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La Scola B., Holmberg M., Andersson S.G.E.;
The louse-borne human pathogen Bartonella quintana is a genomic
derivative of the zoonotic agent Bartonella henselae.";
Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721 (2004).
BRIS. MSS97689; CARZ6991.1; -; Genomic DNA.
GO; GO:0003124; F:catalytic activity; IEA.
GO; GO:0003125; P:metabolism; IEA.
FinterPro; PROD01736; PLD.
Fam: PPO0644; PLDC; 2.
SMART; SM00155; PLDC; 2.
PROSITE; PSS0035; PLD; 2.
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MetHisGlyLeuArg-----LeuPheArgSerSerLysAlalleLeuHisThrLys
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| AsnAsnArg11eTyrTrpAspPheI1eGluAsnGluLysGlnTyrSerI1eAspTyrGlu
   LysValAlaLysValTyrLeuAspTyrValLysGluHisIleAsnPheAspCysPheIle
                                                                            CAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGGCTGATCAGCGACACCCCTGCA
                                                                                                                                                                                                                              AAAGGACTCGACCGCGACCGCCAAACCGCCGATTGCCGGGAGG---CTGCAAGACGCG
                                                                                                                                                                                                                                                                                                   LysAlaLeu-----ArgLysLys-----AlaGlyAsnTrpLeuMetLysAla
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STRAIN=ATCC 49882 / Houston 1;
PubMed=15210978; DOI=10.1073/pnas.0305659101;
Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.F.
Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M.,
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05-3UL-2004 (TrEMBLrel. 27, Created)
05-3UL-2004 (TrEMBLrel. 27, Last sequence update)
05-3UL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                            CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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     Pfam; PF00614; PLDc; 2.
SWART; SM00155; PLDc; 2.
COMDSITE; PS50015; PLD; 2.
COMPLETE PTCTECOME; Plasmid.
SEQUENCE 466 AA; 51793 MW;
                                                                                           3.57e-37
812.50
55.4%
42.0%
28.5%
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Query Match:
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||| ||| ||| ||| ::: ::: ||| GluLysValleu---ArgLysAlaGluAsnTrpLeuMetLysAlaLeuSerGlnVal
                                                        CTCAAACAGCCCGAAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCCTACAAAATCC
                                                                                           GGCACAGACGCCACTGGCAAAACTGGTGCAGGACGGCATAGACGTTACCGTCCTGACCAAC
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|GlyThrGlnAsnPheSerAsnLeuValSerLysGlyValAspValLysIleLeuThrAsn
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Arg------beuPheArgSerSerLysAlaSerLeuHisThrLysAlaPheLeuVal
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| PheTrpArgArgAlaPheAlaLysIleIleSerTrpLeuProIleGluSerGlnLeu
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Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 7:331-338(2000).
EMBL, AP003017; BAB54862.1; -; Genomic DNA, GO, GO:0003824; F:catalytic activity; IEA. GO; GO:0008152; P:metabolism; IEA.
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OrderedLocusNames=mlr9675;
Rhizobium loti (Mesorhizobium loti)
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STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
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GO; GO:0008152; P:metabol
InterPro; IPR001736; PLD.
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108 GluvalIleAlaAlaAlaAspArgGlyValArgValArgLeuLeuLeuAspAspLeuGly 127
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8 IleIleIleLeuLeuMetLeuIleGlyProSerLeuPheValValIleGlyLysGlnArg
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                  Markelz
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Planagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., Strub G., "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.", Science 294:2312-2328(2001).

EMBL, AE008120, AALA5321.; -, Genomic DNA.

EMBL, AE008085, AAK87408.1; -, Genomic_DNA.
                                                                                                                                                                                                                                                                         F08804A62B810AE2 CRC64;
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204
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                 GO; GC:0003824; F:catalytic activity; IEA.
GO; GC:0008152; P:metabolism; IEA.
Horerpo; IPR001736; P.D.
Pfam; PF00614; PLDc; 2.
SMART; SM00155; PLDc; 2.
PROSITE; PS50055; PLD; 2.
COMDIEC protecome.
SEQUENCE 518 AA; 58096 MW; F08804A62B8
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PIR; G97556; G97556.
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DB:
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AlaSerLeuHisThrLysAlaPheSerValAspAspArgIleGlyPheValGlySerPhe
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LysLeuValMetGluLeuArgHisArgPheLysSerGluThrAlaProGluAlaSerTyr
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
                                                CATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gordon D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804; Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Cahang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Cordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBJUEX3 AGRT5 PRELIMINARY; PRT; 518 AA.
00UEX37 Q7CYU7;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Phospholipase D family protein (AGR C 3007p).
OrderedLocusNames=AGR C 3007, Atul630;
OrderedLocusNames=AGR (S 07) Atul630;
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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NCBI_TaxID=176299;
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Takeuchi C., Yamada M., Tabata S.;

Takeuchi C., Yamada M., Tabata S.;

Takeuchi C., Yamada M., Tabata S.;

Takeuchi C., Yamada M., Tabata S.;

Mochizobium loti.";

DNA Res. 7.331-338(2000)

REMBL; BA000012; BAB53717.1; -; Genomic DNA.

GO; GO:0003824; F:catalytic activity; TEA.

GO; GO:0003824; F:catalytic activity; TEA.

RITERPRO; PRO01736; PLD.;

RITERPRO; PRO01736; PLD.

RYART; SM00155; PLDC; 2.

RYART; SM00155; PLDC; 2.

RYART; SM00155; PLD; 2.

RWART; SM00155; PLD; 2.

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Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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Matches:
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MEDLINE=21082930; PubMed=11214968;
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                                        -GCCACG
                                                                                                                                                                                                                                                                                                                             ||| |||||| || |||||| | :: ||||||| | :: AspAspTyrTrp-----AsnSerAlaValSerValProValArgSerLeuLeuAlaArg
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--------SerGlnAlaAspGlnGlySerPheThrLeuArgGlySerGlyGln
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                                                                                                                                                           CGCATCATCCGCAGCGCAACATCGGCAAGGGTCTTCAAGCACTCGGGATACAACGACGAA
                                                                                                                                                                                                          ArgProAsnLysLeuAlaLysLeuArgArgGluLeuAspAlaLeuProGlnSerGlu---
                                                                                                                                                                                                                                                                                       ACATCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGTCGCCCCTCTACCAA
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ProLeuValAlaArgMetAspGluIlePheAlaGluGluIleArgArgThrMetSerPhe
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ArgLeuGlnThrTyrThrArgGluProGluAlaAlaTrpPheArgArgIleLeuAlaAla
                                                                                                                                                                                                                                                                                                                                                                      280 GlulleValSerProTyrPhelleProGlyLysGlySerLysIleLeuGlyAspLeu
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                           ----LysProileAlaGluLeuGlyAlaAlaAlaPro
                                                                  791 ACATCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGTCGCCCCTCTACCAA
                                                                                        |||| :::||| |||| GlySerHisAlaProTyrPheGluGlyArgGluGluLysThrGluSerThrLeuLeuSer
                                                                                                                                        851 AAAATACAG-----AGGGACGCATCGACTGG
                                                                                                                                                                         GlyileArgAspLysGlySerIleAlaGluPheIleSerAlaSerSerAsnValHisTrp
                                                                                                                                                                                                           CAGAGCGTCCAAACCCGCCTGATCAGCGACCCCTGCAAAAGGACTCGACCGCGACGCC
                                                                                                                                                                                                                                                242 ValGlu---ArgValArgValIleSerAspProProGluLys---ValArgGlyTrpArg
                                                                                                                                                                                                                                                                                 938 CGCAAACCGCCGATTGCCGGGAGGCTGCAAGACGCGCTCAAACAGCCGCGAAAAAAGCGTC
                                                                                                                                                                                                                                                                                                                    260 ProArgSerTrpLeuMetLysGluLeuLeuProIleIleGlnSerAlaArgLysArgval
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Putative phospholipase D protein.
OrderedLocusNames=ACIAD1881;
Adinetobacter sp. (strain ADP1).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Noraxellaceae; Acinetobacter.
NCBL_TAXID=62977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCCTATCCCTGCTGCCCATCGAAGGTTTATTA 1561
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LeuValArgHisLeuProIleGluSerGlnLeu 466
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QGFB53;
QGFB53;
O5-UUL-2004 (TYEMBLE1. 27,
05-JUL-2004 (TYEMBLE1. 27,
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AC 06 FB5
AC 06 FB5
DT 05-JU
DT 05-JU
DT 05-JU
DT 05-JU
CO 05-JU
CO 00 ACI
CO MOCAN
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415

68

88

535

595

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MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
A darber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
A Garber R.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
A Endy L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
A smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
A Reizer J., Saler M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
T. (Complete genome sequence of Pseudomonas aeruginosa PAOI, an
Copportunistic pathogen.",
A Rabi, AE004943; AA608695.1; -; Genomic_DNA.
BRB, AE04943; Frizansferase activity; IEA.
GO, GO:0016740; Frizansferase activity; IEA.
GO, GO:000654; Prhospholipid biosynthesis; IEA.
BREAPPORTUSS, PLDC; Z.
SWART; SM00155; PLDC; Z.
BRART; SM00155; PLDC; Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 CATAACAACGGGCTATCCGACATCTACCTGCTCGACGACCCCCACGAAGCCCTTGCCGCC 250
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|HisAsnLysLeuTrpLeuAlaAspGlyThrAlaAlaIleValGlyGlyArgAsnLeuGly 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCAGCCTCATTTCCCTTTTATGCCTCCTTCTTCTTCATGTTCTTCATGGTTGCCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome; Hypothetical protein.
SEQUENCE 529 AA; 59199 MW; DABFSED5881E63DE CRC64;
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200
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189
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Matches:
Conservative:
Mismatches:
Indels:
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52.5%
36.7%
27.8%
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Best Local Similarity:
Query Match:
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LysGlnArgTyrSerValLysTrp-----AlaLysAlaHisPheValAlaAspSerPro
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| LystysileHisGlyHisAlaIleGlyAsnGluLeuIleTyrAsnGlnMetPheSerIle
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                                                914 GCAAAAGGACTCGACCGCGGACCGCCGCAAACCGCCGATTGCCGGGAGGCTGCAAGACGCG
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                                                                                                           -------TGGCAGAGCGTCCAAACCCGCCTGATCAGCGACACCCCT
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadacee; Pseudomonas.
VCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395 ThrTrpTyrGluLysMetThrGlyArgValIleProAla-------
                      -----TCGCCCCTCTACCAAAAATACAGACGGGACGCATCGAC-
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|MetLysAlaValSerTyrLeuProlleGluTrpMetMet 520
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] TOUCLEOTIDE SEQUENCE.
STRAIN=ATCC 15692 / PAO1;
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Q9HTP4;
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286 LeuGlyAsnTrpLeuGluAsnLeuThrTrpAlaArgAlaGluAlaileTrpAspAlaPro 305
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266 GluSerValLysGluSerGlyTyrIleArgHisLeuPheAspArgGlyAspGlnProArg
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24 ArgAlaLeuValLeuCysAlaAlaLeuAlaLeuSerGlyCysAlaThrHisProProAla
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X PubMed=1537793; DOI=10.1073/pnas.0403306101;

A Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,

A Feldblyum T.V., Ulrich K.L., Ronning C.M., Brinkac L.M.,

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Zafar N., Zhou L., Fraser C.M.;

Richt C., Structural flexibility in the Burkholderia mallei genome.";

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R STIGK: BMAA0208;

TIGK: BMA
                                                                                                                                                                                                                                                                   Burkholderia mallei (Pseudomonas mallei).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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| AlaPro-----ArgGluThrSerGlnAlaLeuProAlaHisGluSerAlaPheGly 41
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DOI=10.1046/1.1462-2220.2002.00366.x;
Doi=10.1046/1.1462-2220.2002.00366.x;
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Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
 ||| ||| ::: ||| ::: ||| LeuvalTrpThrGluIleAlaAspGlyGlnValArgThrTyrSerValAspProAsnAla
                                                     1502 AAACTTTGGAAACGCATCGCCGCAAAAATCCTATCCCTGCTGCCCATCGAAGGTTTATTA
                                                                             GlyPheTyrArgAsnLeuLhrGlyLeuCysLeuLeuLeuProlleAspAspGlnLeu
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ArgAlaLeuProLeuLeuLeuValLeuLeuLeuGlyValAlaGlyCysThrSerIleSer
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                                                                                                                                                                                                                                                                       Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metabolically versatile Pseudomonas putida KT2440.";
Environ. Microbiol. 4:799-808(2002).
EMBL; AE016793; AAN70841.1; -; Genomic_DNA.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Phospholipase D family protein.
OrderedLocusNames=PP5276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO, GO:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008654; P:phospholipid biosynthesis; IEA.
InterPro; IPR001736; PLD.
Pfam; PF00614; PLDC; 2.
SMART; SM00155; PLDC; 2.
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Matches:
Conservative:
Mismatches:
Indels:
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SEQUENCE 517 AA; 57574 MW;
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53.68
37.88
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Q88CAS;
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Best Local Similarity:
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                            PheAsnProPheGlyAlaProArgLeuGlyMetPheAlaArgThrAlaAsnValPheThr
                                                             GACTTCCCCCGCCTCAACCGCCGCATGCAAAAAATCCTTTACCGCCGACAACCGCGCC
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TTCAACCCCTTCGTCCTACGCAAATGG--
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1544 CCCATCGAAGGTTTATTA 1561
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540 AA; 59105 MW;
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772.50
52.2%
36.8%
27.1%
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Q4LJD9;
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity:
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PheValProGlyGluProGlyLeuLeuTyrLeuThrGlyArgAlaAspAlaGlyValSer
                                            ACCGACTTCCCCCGCCTCAACCGCCGCATGCACAAATCCTTTACCGCCGACAACCGC
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200 AsnPheThrAspIleAspLeuLeuGlyValGlyProValAlaGluGlnLeuGlyHisSer
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1376 CAGATGGAGCGCACCCTCGCCGAT----ACCACACCCGAATACGCCTACCGCGTTACC 1429
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| GlnAlaArgAlaLeuValValCysAlaLeuLeuProLeuAlaAlaAysAlaThrHisPro
                          CGTTCCGCACGGCTCAATACCGAAATGGGCGTCGTCATCGAAAGCCCCAAAATCGCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=HI2424;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cenocepacia
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Burkholderia cenocepacia H2424.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HI2424.";
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Phospholipase D/Transphosphatidylase precursor.
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Matches:
Conservative:
Mismatches:
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EMBL; AAHL01000070; EAM16198.1; -; Genomic_DNA
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STRAIN=H12424;
US DOE Joint Genome Institute (JGI-ORNL);
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41 Prolitativescleuksprigprovalishilahlacusshildolumkhlamker 60  158 (TroacolounterCorcolounterCorcolounterCorpolauchachachachachachachachachachachachachac	Db 186 ValAlaValGInSerGIYTYRAIRPTOTYRAGVAIPPOLACUGUGIANTGGIYVAIGIU 405  Oy 1175 CTCTRCAGCCTCCAACCACCACCACCCCCCCCCCCCCCCC	lign ore
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| HetalaTyrLysThrGlnProArgMetLysThrTrpLeuAsnGluLeuValTrpAlaHis 306
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                                                                         ------GGACAACATCCTG 172
                                                                                                                                                           CAAATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACGACCCC 232
                                                                                                                                                                                                                                            CAATACTACATTTGGCGCAACGACATTTCCGGCAGGCTGCTGTTCAACCTCATGTACCTT 352
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CysLeuLeuValAlaValCysValSer-GlyCysAlaHis-GlnGlnIleAlaSerGluP
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| roSer------GlnAlaMetProProSerAspSerAlaPheGlyArgSer-Ile
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Conservative:
Mismatches:
Indels:
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                                                                                                                  CGTCATTTCAATACTTCCAAACCTGTCCTCCT
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1183 1495 CTG-----CAACCCAACCATGCCGTCCCCCCACAAAGACAAAGGCCTGACCGGC--- 1234 1496 GAAGCCAAACTITGGAAACGCATCGCCGCAAAAATCCTATCCCTGCTGCCCATCGAAGGT 1555 422 -----AGCTCCGTAACCAGCCTGCATGCCAAAACC 1264 1265 ITCATIGIGGACGCAAACGCAICITCAICGGCTCATICAACCICGACCCCCGTTCCGCA 1324 1382 GAGCGCACCCTCGCCGATACCACACCCGAATACGCCTACCGCGTTACCCTCGACAAACAC 1441 540 LeuLeuLeuThrThrGlnLeuAlaProGluLeuLeuAsnThrArgLysGluLeuMetLeu 346 406 ---GlyAspTrpTrpArgArgPheAsnAlaTrpMetSerArgAlaIleGlyLeuGluArg GTTTCACCCTATTTCGTCCCTACAAATCCGGCACAGACGCCACTGGCAAAACTGGTGCAG CATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAG GlubeuthrieuGlnGlyMetAlaProSerLeuThrTyrGluAlaArgLeuGlu---Asp 1442 AACCGCCTGCAATGG-----CACGATCCCGCCACCCGAAAAACCTACCCGAACGAACCC 502 GlyLysValValTrpValThrGluAspAsnGlyGlnIleHisThrLeuHisThrGluPro -------------TTATTA 1561 542 :::||| MetLeu 483 ( 407 1325 1184 1235 522 327 1124 423 443 qq g g QQ \triangle \trian 8 G ò 8 Q ò ò 8

Search completed: May 2, 2006, 05:24:25 Job time : 460 secs

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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                 Copyright
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OM nucleic - protein search, using frame\_plus\_n2p model

2, 2006, 05:12:46 ; Search time 12.2 Seconds (without alignments) 2462.203 Million cell updates/sec Мау Run on:

US-10-665-990A-13 2852 Title: Perfect score:

1 caaaatacaggcaatgccgt.....tgcccatcgaaggtttatta 1561 **BLOSUM62** Scoring table: Sequence:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

-MODEL-frame+ n2p.model -DEV=xlp
-Q=Abss/ABSSWEB spool/US10665990/runat\_01052006\_111946\_9536/app\_query.fasta\_1
-Q=Abss/ABSSWEB spool/US10665990/runat\_01052006\_111946\_9536/app\_query.fasta\_1
-DB=PIR -QFWT=abstan -SUFFIX=pr -MINMATGH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pc-1 -THR MAX=100 -THR MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=ppc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02p
-USER-SIO665990 @CGM 1 1 63 @runat\_01052006\_111946\_9536 -NCPU=6 -ICPU=3
-NO MWAP -NGG SCÖRES=0 -MAIT—DSPBLÖCK=100 -LONGLOG -DEV\_TIMEOUT=120
-WARN TIMEOUT=30 -THRRADS=1 -XGAPPOP=10 -XGAPPEXT=0.5 -FGAPPOP=6 -FGAPPEXT=7
-YGAPPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	phopholipase D-fam	cardiolipin synthe	ymdC protein - Esc	probable synthase	probable synthase	conserved hypothet	hypothetical 55.9K	phospholipase D fa	conserved hypothet	probable cardiolip	conserved hypothet	cardiolipin syntha	mucin 2 precursor,	glucan 1.4-alpha-q
	ı QI	B81859	B81083	C64847	H90806	D85666	AE0636	G97556	AB2777	F82983	E71963	F64543	B82724	A43932	S48478
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	Query Match Length DB	525	508	493	493	493	495	518	518	529	502	502	652	3020	1367
dю	Query Match	92.2	90.2	38.7	38.6	38.3	38.2	28.3	28.3	27.8	22.2	22.0	15.4	11.8	11.3
	Score	2630	2573	1102.5	1100.5	1093.5	1089.5	807	807	792	632	627	439	336.5	323.5
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G70063	F90001	AI1433	147141	T45462	T45463	A11075	AI1762	AG1387	T45025	906685	H86744	B84007	C84125	T43863	H82711	T02345	B82971	860089	VGBEX1	AE3539	E97307	D83103	AH2333	T43481	S21054	138186	90	A27677	JH0557	S57180
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15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

PARACESSION: B81859
C; Species Neisseria meningitidis
C; Species Neisseria meningitidis
C; Species Neisseria meningitidis
C; Species Neisseria meningitidis
C; Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004
C; Accession: B81859
R; Parkhill, J; Acthuman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morc.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrean, Nature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A; Reference number: A81775; MUD:2022556; PMID:10761919
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-525 cPRR>
A; Residues: 1-525 cPRR>
A; Cross-references: UNIPROT:09JTT1; UNIPARC:UP1000005033F; GB:AL16756; GB:AL157959; NI
A; Gene: NMA1646
C; Superfamily: cardiolipin synthase

Alignment Scores:			
Pred. No.:	8.8e-147	Length:	525
Score:	2630.00	Matches:	509
Percent Similarity:	98.78	Conservative:	4
Best Local Similarity:	97.9%	Mismatches:	7
Query Match:	92.2\$	Indels:	0
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US-10-665-990A-13 (1-1561) x B81859 (1-525)

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	RESULT 3  C64847  ymdC protein - Escherichia coli (strain K-12)  C;Species: Bacherichia coli C;Species: L2-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004 C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004 C;Accession: C64847 R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A;Reference D.J.; Nau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUD:97426617; PMID:9278503 A;Reference number: A64720; MUD:97426617; PMID:9278503 A;Accession: C64847 A;Status: nucleic acid sequence not shown; translation not shown A;Status: nucleic acid sequence not shown; translation not shown A;Residues: 1-493 *cBLAT> A;Cross-references: UNIRROT:P75919; UNIPARC:UPI0000138993; GB:AE000206; GB:U00096; NID A;Experimental source: strain K-12, substrain MG1655 C;Genetics: A;Genetics:  Alignment Scores: 3.32e-57 Length: 493  Pred. No.: 1102.50 Matches: 221  Score: Percent Similarity: 65.5\$ Conservative: 83  Best Local Similarity: 47.6\$ Mismacches: 143  Query Match: 2 Gaps: 5	US-10-665-990A-13 (1-1561) x C64847 (1-493)  Qy	
278 CACAGCCTCGATTTGCAATACTACATTTGGGGCCAACGACATTTCCGGCAGGCTGCTTC 337	CCCCGCCTCAACCGCCGCATGCACAAATCCTTTACCGCCGACACCGCCCACTA 5 ProArgLeuAsnargArgMetHisAsnLysSerPheThralaAspAsnArgAlaThrIIe 1 CTCGGCGCACCATATCGCCGACCACAAATCCTTTACCGCCGCCACCATA 5 ProArgLeuAsnargArgMetHisAsnLysSerPheThralaAspAsnArgAlaThrIIe 1 CTCGGCGCACGCAATACTTCAAAGTCGGTGAGGACACCGTTTTCGCC 6	818 CGCGAAACCGTCGAACAGTCGCCCCTTACCAAAAATACAGACGGACG	938 CGCAAACCGCCGATGCCGGAGGCTGCAAGACGCCCCAAAAAACCGCTCAAAAAACCGCTCAAACCGCCCGAAAAACCGTTTCATCCTCCTAAATCCGGCACACACGCCACACGCCACACGCACACGCCAAAACTC 1057

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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H90806
R;Hayashi, T:; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genon
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genon
A;Reference number: A99629; MUID:21156231; PMID:11258796
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ore: 1093.50 Matches: 219 St. Local Similarity: 65.3\$ Conservative: 84 St. Local Similarity: 47.2\$ Mismatches: 144 ery Match: 2 Gaps: 5 -10-665-990A-13 (1-1561) x D85666 (1-493)	37 37 260		3 80 C	440 CATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCTACGCAAATGGCGCGCACTC 49	500 137 560	157 AspGlyvalValThrGeCGACCTGGACATCGCGACGGCACGGCAGGGCGTCGTCGTAGGTAG	::: :::   ::	:::		234 HisAsnAspAlaMetThrHisArgTyrLeuArgLysWetGluSerSer 249  839 CCCTCTACCAAAAATACAGACGGACGCATCGACAGGCGTCCAAACCCGCCTG 898	899 ATCAGGGACACCCTGCAAAAGGACTCGACCGCGCGCGCAAACCGCCGATTGCCGGG 958 :::	959 AGGCTGCAAGACGCGCTCAAAAGGCGTCTATCTGGTTTCACCCTATTTC 101 	1019 GTCCCTACAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGACGGCATAGACGTT 1078	1079 ACCGTCCTGACCAACTCGCTACAGGCGACCGACGTTGCGCCCTTCCGGCTACGTC 1138	1139 AAATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCAACCAT 11
269 958 289 1018		1138		38 13		TCGAC 1435       euAsp 449	CGAAC 1489 ysLys 469	CCATC 1549   ::: roVal 489		.i (strain 0157:H7, substrain EDL933) QY #text_change 09-Jul-2004 Db	J.; Mayhew ; Apodaca,		OY 1165766; GB:AE005174; NID:G12514578; F 11933 DD	λό dd	493 Qy
250 ProPhelleAsnHisLeuValAspGlyThrLeuProLeulleTrpAlaLysThrArgLeu 899 ATCAGCGACACCCTGCAAAAGGACTCGACCGCGCACCCGCAAACCGCCGATTGCCGGG :::	290 ArgLeuPheAspileMetGlySerFroSerGluArgileAspileileSerSerTyrPhe 1019 GTCCCTACAAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGACGGCATAGACGTT		1139 AAATACCGAAAACCGCTGCTCAAAGCCGGCATCAACTCTACGAGCTGCAACCCTTCTACGAGCTGCAACCAT :::::	370 GluGlnSerSerThrLeuHisAspArgGlylleThrGlyAsnSerGlyAlaSerLeuHis 1256 GCCAAAACCTTCATTGTGGACGCCAAACGCATCTTCATCGGCTCATTCAACCTCGACCCC	390 AlaLysinrPheSerileAspGlyLysThrValPheIleGlySerPheAsnPheAspPro 1316 CGTICCGCACGCTCAATACCGAAATGGCCTCGTCATCGAAAGCCCCAAAATCGCAGAA  1316 L      1		1436 AAACACAACGCCTGCAATGGCACGATCCCGCCACCCGAAAAACCTACC :::	1490 GAACCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATCCTATCCCTGCTGC	1550 GAAGGTTTATTA 1561               490 GluTrpLeuLeu 493	RESULT 5 D85666 probable synthase ymdC [imported] - Escherichia coli (strain O157:H7, substrai C;Species: Escherichia coli C;Species: Dscherichia coli C;Apecies: Dscherichia coli C;Apecies: Dscherichia coli C;Apecies: Dscherichia coli C;Apecies: Dscherichia C;Apecies: Dscher	a, N.T.; Plunkett III, G.; Burland, V.; Mau, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Di. 409, 529-513, 2001  e: Genome sequence of enterohemorrhagic Esche	rence number: A85480; MUD:21074935; PMID:112 ssion: D8566 Las preliminary cule type: DNA	uues: 1-493 <sto> s-references: UNIPROT:Q8X917; UNIPARC:UPI0000 timental source: strain O157:H7, substrain ED tics:</sto>	ene: ymdC uperfamily: cardiolipin synthase	Alignment Scores: Pred. No.: 1.12e-56 Length:
9 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 & 8	اري دي دي	ሪ 8 ሪ	a & a	g & g	S G	Oy Dp	oy B	<u>ئ</u> ۾	RESULT D85666 probab C;Spec C;Date	R; Pern iller, Nature A; Titl	A;Refe A;Acce A;Stat A;Mole	A, Kesidues: A, Cross-ref A, Experimer C, Genetics:	A;Gene C;Supe	Alignm Pred.

	1133 TACGTCAAATACCGAAACCGCTCCAAAGCCGGCATCAACTCTACGAGCTGCAACCC   1192
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	6 6 6 6 6 6 6 6
Db 330 ArgTrpArglyeiseLeuLeuArgryrGlyvalGluEeuTyrGluEeuLysProTheArg 369  330 ArgTrpArglyeiseLeuLeuArgryrGlyvalGluEeuTyrGluEeuLysProTheArgcTACCTCCT 1255  330 GluGInSerSerThrLeuHiaAspArgGlyIleThrGlyAsnSerGlyAlaSerIeHia 389  330 GluGInSerSerThrLeuHiaAspArgGlyIleThrGlyAsnSerGlyAlaSerIeHia 389  330 AlaCymThrPhoSerIeLeaArgCACCCTTCTCCACCTCCAAACCTCCAAACCT 135  410 AlaCymThrPhoSerIeLeaArgCACCCCATTCTCAAACCCCCAAAACCTACAAA 1375  410 AlaCymThrPhoSerIeLeaArgCACCCAAAACCTCTCCAAAACCCCCAAAACCTACCCCAAAA 1375  410 AlaCymThrPhoSerIeLeaArgCACCCCAAAACCCCCCAAAACCAAAACCCCCCAAAACCAACCCC	Alignment Scores: 1.92e-56

430 AlaThrLeuIleHisLysArgPheThrGlnSerGlnArgAspAlaAlaTrpGlnLeuArg 449  1430 CTGGACAAACACACGCCTGCAATGGCACGATCCGGCCACCGGAAAAACCTAC 1483	461 CTGTTCAACC              148 LeuPheAsnP       512 GACTTCCCCC 	CTGTTCAACCCCTTCGTCCTACGCAAATGGCGCGCACTCGGCTACCTGACC
rgLeuAlaAlaIleLeu 489	572 ACCATACTCG         :::     188 ValileValG	ACCATACTCGGCGGACGCAATATCGGCGACGAATACTTCAAAGTCGGTGAGGACCCGTT
region [imported] - Agrobacterium tum #text_change 09-Jul-2004	208 PhenisABPhe. 692 GACCGCTACTGG 228 ASPASDTYTTP	
Rigodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2338, 2001 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:2160851; PMID:11743194	731 CGCATCATCC    : 246 ArgProAsnL	CGCATCATCCGCAGCGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAA
A;Accession: G97556 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-518 «KUR» A;Residues: 1-518 «KUR» C;Generics: UNIPROT:Q8UEX3; UNIPARC:UPIO0000D1C0B; GB:AE007869; PIDN:AAK87408.1;		ACAILCASAGAS CONTROL OF THE CONTROL OF THE CANAL OF THE C
	279 ArgAspHisP 899 ATCAGCGACA ::::::	ArgasphispheLeuMetSerAspArgLeuHisTrpValAspThrAlaAspVal ATCAGCGACACCCCTGCAAAAGGACTCGACCGCGACCGCGCAAACCGCCG ::::            :::
518 204 85 196		DeuniansproficolioniungstaanidulybysArgarglybelyhisasnirheleu GCCGGGAGGCTGCAAGACGCGCTCAAACAGCCCCGAAAAAGCGTCTATCTGGTTTTCACCC 
		TATTTCGTCCTACAAATCCGGCACAGACGCACTGGCAAACTGGTGCAGGACGCCATA       ::
CTCATTTCCCTTTTANGCCTCCTTCTTGTTCATGTTCTTCANGCTTGCCCCCACTGGAA 112 :::                   ::	1073 GACGTTACCG ::: : 356 SerLeuAlaI	GACGTTACCGTCCTGACCAACTCGCTACAGGCGACCGACGTGCCGCCGTCCATTCCGGC ::: ::
GAACGGACGGAAAGCCGTCATTCAATACTTCCAAACCTGTCCTCGGACAACATCCTG 172    ::: :: :: ::		TACGTCAATTACCGAAAACCGCTGCTCAAAGCCGGGATCAACTCTACGAGCTGCAACCC     :::
CAAATCCGGCACCCCTCATAACAACGGGCTATCCGACATCTACCTG 220		AACCATGCCGTCCCGGCCACAAAAGACAAAGGCCTGACCGGCAGCTCCGTA :::
CTCGACGACCCCACGAGCCCTTGCCGCCGCCGCCCTTATCGAATCTGCCGAACAC 280	1244 ACCAGCCTGCJ         410 AlaSerLeuH	ACCAGCCTGCATGCCAAACCTTCATGTGGACGGCAAACGCATCTTCATCGGCTCATTC
rgrrcaac ::	1304 AACCTCGACCC          430 AsnPheAspP?	AACCTCGACCCCCGTTCCGCACGGCTCAATACCGAAATGGCCGTCGTCATCGAAAGCCCC
	1364 AAAATCGCAGA ::: 450 ProLeuValAl	AAAATCGCAGAACAGAGGCGCCCCCCCCGATACCACCCCGAATACGCCTAC :::       :::       :::       :::         :::           :::
	1421 CGCGTTACCCT ::: 470 GluLeuAspI	CGCGTTACCCTCGACAAACACACCCCTGCAATGGCACGATCCCGCCACCCGA ::: ::          ::     CluLeuAspIleAspSerAlaAsnArqIleValTrpMetThrGluGluArqGlyGlnPro
sProAsnIleGluLeuArg 147	1475 AAAACCTACC	1475 AAAACCTACCGGAACGCAAGCCGAAGCTTTGGAAACGCATCGCCGCAAAAATCCTA 1534

GACTICCCCGGCCTCAACCGCGCATGCACAACAATCCTTTACCGCCGACACCGGCCCAPGPACACACATACCAACCGCGCCCCAACACCGCGCCCAPGCACAATACCGCGCCCCACATACCGCGCCCCAACACCGTT valllevalGlyGlyArgArancGCCACCACATATCCACACCATACCGCGCCCCTTCCCCCGCCACCTTCCCCCCCC	430 AsnPheAspProArgSerAlaSerLeuAshThrGluMetGlyValValPheAsnSerAla 449  1364 AAAATCGCAGAACAGATGGAGCCCCCCGCGATACCACCCGAATACGCCTAC 1420  :::      :::      :::      :::      :::        :::
<ul><li>6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B</li></ul>	B & B & B & B
99 1935 TCCTCTCTCCTCCAAGGTTATA 1561  8850LT 8	

	286 LeuGlyAsnTrpLeuGluAsnLeuThrTrpAlaArgAlaGluAlaIleTrpAspAlaPro 305 914 GCAAAAGGACTCGACCGCGCCCAAACCGCCGATTGCCGGAGGCTGCA 967	1028 AAATCCGGCACAGACGCACACACCTGCCACACACCCCCACACACCCTCTCT 1087 346 LysAspGlyLeuAsnTyrLeuThrGlyLysAlaAspSeTGlyValargValaArgLeuLeu 365 1088 ACCAACTCGCTACAGCCGACCGACCTGCCCTCCTTCCGGCTACACTCAAATACCGA 1147 366 ThrAsnSerLeuGludlaThrAspValProAlaValHisAlaGlyTyrAlaPrOTyrArg 385 1148 AAACCGCTGCTCAAAGCCGACCATCCCACCACCACCACCACCACCACCACCACCACCAC
8 8 8 8 8 8 8 8 8 8		6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6
Oy 1535 TCCCTGCTGCCCATCGAAGGTTTATTA 1561  Db 510 ArgValLeubroLeuGluSerGlnLeu 518  RESULT 9  F82983  Conserved hypothetical protein PA5310 [imported] - Pseudomonas aeruginosa (strain PAO1)  C; Species: Pseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C; Accession: F82983  R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 200 A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A; Reference number: A82950; MUID:20437337; PMID:10984043 A; Accession: F82983 A; Acc		10   ArgargheleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLe

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Conserved hypothetical secreted protein HP0190 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: F64543
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKennc Peterson, S.; Loftus, B.; Richardson, D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTTCATCGGCTCATTCAACCTCGACCCCGTTCCGCACGCTCAATACCGAAATGGGC 1345
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                                            PhelysAsnGlnIleSerLysGlyIleGluLeuAsnIleLeuThrAsnSerLeuSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||::: :::::||| ||| ||| ||| ValLeuPheAspAsnProScrPheAlaLysArgValArgLeuSerLeuLysAspHisAla
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                                                                                              AACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAAACATCCAGACACGCGCTC
                                                                                                                                                                            CTGCGCTACCGCGAAACCGTCGAACAGTCGCCCCTCTACCAA----AAAATACAGACGGGA
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                  TCCGCCCACACGCCACGCGCATCATCCGCAGC-
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probable cardiolipin synthase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Decies: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: E71963
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ivee, C.; Gibbon, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUD:99120557; PMID:9923682
A;Accession: E71963
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Db 265 LysValAsnAsphelleAspArgPheGlnLysTyrGlnTyrProlleTyrTyrGlyAsn 284  Qy 899ATCAGCGACACCCCTGCAAAAGACTCGACCGCGACCGCCGAAACCGCCG 949  285 AlallePheLeuAlaAspSerProLysLysIleAspThrProLeuTyrSerPro 302  Qy 950 ATTGCCGGCAGGCTGCAAACAGCCCTCAAACAGCGCTTATCTCTCTTTTA 1009	323 SerTyrPhelleProGlyLysLysMetMetLysllePheLysanGlnIleSerLysGly 1070 ATAGACGTCCTGACCAACTCGCTACAGCGACGTTGCCGCCGTCCTTCC 1431 lleGluLeuAsnlleLeuThrAshSerLeuSerSerThrAshAlallevalValTyrGly		1190 CCCAACCATGCCGTCCCGCCACAAAAGACAAAAGGCCTGACCGCAGCTCCGTAACCAGC :::         ::	1250	Qy 1310 GACCCCGTTCCGCACGGCTCATACCGAAATGGGCGTCGTCGTCGAAAGCCCCAAAATC 1369	Qy 1370 GCAGAACAGATGGAGCGCACCTCGCCGATACCACCCGAATACGCCTACCGCGTTACC 1429		Oy 1490 GAACCCGAAGCTTTGGAAACGCATGGCGGAAATCCTA 1534	RESULT 12 B82724 cardiolipin synthase XF1087 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa	C;Accession 182724 C;Accession 182724 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque Nature 406, 151-157, 2000	A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below A;Accession: B82724	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-652 <sim> A;Cross-references: UNIPROT:Q9PEE1; UNIPARC:UPI00000C2600; GB:AE003945; GB:AE003849; NI</sim>	A, Experimental source: strain 9a5c R, Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, as-Neco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.	submitted to GenBank, June 2000 A; Athabors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.P.; Krieger, J.B.; Kuramae, E.E.; Laig J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laig chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.S.; Martins, C.L.; Marques, M.V.; Martins, A; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D
arence number: A64520; MUID:97394467; PMID:925218 ssion: F64543 tus: preliminary; nucleic acid sequence not shown ecule type: DNA sequences: UNIPROT:P56117; UNIPARC:UP10000139 ss-references: UNIPROT:P56117; UNIPARC:UP10000139 rt codon: TrG rt codon: TrG rt codon: TrG nent Scores: 2.56e-29 Length:	: 627.00 nt Similarity: 48.9% Local Similarity: 31.5% Match: 22.0%	US-10-665-990A-13 (1-1561) x F64543 (1-502) Qy	8	Qy 254 GCCGCCCTTATCGAATCTGCCGAACACAGCCTCGATTTGCAATACTACATTTGGCGCAAC 313	Qy 314 GACATTTCCGGCAGGCTGCTGTTCAACCTCATGTACCTTGCCGCAGAACGCGGGGTGCGC 373	Qy         374 GTACGCCTGCTGTTGGACGACAACAACAACGGGGGTTGGACGATCTC 421	Oy 422 CTGCTCGCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTGGTCCTA 481 :::	Qy     482 CGCAAATGGCGCGCACTCGGCTACCTGACCGACTTCCCCCGCCTCAACCGC 532	Oy 533 CGCATGCACAACAAATCCTTTACCGCCGACAACCGCGCCCACATACTCGGCGGACGCAAT 592	Oy 593 ATCGGCGACGAATACTTCAAAGTCGGTQAGGACACCGTTTTCGCCGACCTGGACATCCTC 652	Qy 653 GCCACCGGCAGGTCGTCGGCGAAGTATCGCACGACGCTACTGGGCAAGCCAT 712	Qy 713 TCCGCCACAACGCCACGCGATCATCCGCAGCGCAACATCGGCAAGGGTCTTCAAGCA 772 ::: ::::   ::: Db 225 ArgSerIleProValSerLeuLeuArgThr234	Qy 773 CTCGGATACAACGACGACACGCGCTCCTGCGCTACCGCGAACCGTCGAA 832	Oy 833 CAGTCGCCCTCTACCAAAAATACAGACGGGACGCATCGACTGGCAGGCGTCCAAACC 892 :::     ::::

Db 299 PheValAspProAlaLeuAlaValAsnLysValGlnTyr	OY 1016 TTCGTCCCTACAAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGACGGC 1069  352 LeuValLeuSerLysProAlaLeuAsn1lePheArgArgLeuAsnArgThrdlnAspLys 371  OY 1070 ATAGACGTTACCGTCCTGACCAACTCGCTACAGCGACGACGTTGCCGCCCTCCATTCC 1129  172 ProArgValValValValThrAsnSerLeuAlaAlaThrAspAsnPro1leValTyrAla 391	Qy         1130 GGCTACGTCAAATACCGAAAACGGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTG 1186           Db         ::	Qy         1192	Qy         1243	1283 512 1343		Db 561AlabroArgLysLeuProGlyLeuTyrLysLeuAshTyrSerValGlyLys 578  Qy 1505 CTTTGGAAACGCATCGCGCAAAAATCCTATCCTGCTGCCC 1546  Qy 1505 CTTTGGAAACGCATCGCGCAAAAATCCTATCCTGTGCCC 1546          ::-	RESULT 13 A43932 mucin 2 precursor, intestinal - human (fragments) N;Alternate names: mucin SMUC-41 C;Species: Homo sapiens (man) C;Date: 10-Mar-1993 #sequence revision 12-Apr-1996 #text change 31-Dec-2004 C;Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329 R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.	J. Biol. Chem. 269, 2440-2446, 1994 A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the A;Reference number: A49963; MUID:94132002; PMID:8300571
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvair M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328 A;Contents: annotation C;Genetics: A;Genetics: C;Superfamily: cardiolipin synthase	Alignment Scores: 2.76e-18 Length: 652 Score: 439.00 Matches: 161 Percent Similarity: 40.1% Conservative: 69 Best Local Similarity: 28.0% Mismatches: 200 Query Match: 15.4% Indels: 144 DB: 2 Gaps: 21 US-10-665-990A-13 (1-1561) x B82724 (1-652)	125 AGCGGTCATTCAATACTTCCAAA 125 AGCGGTCATTCCAAACTTCCAAA 1	245 GCCGCCCGGCCCTTATCGAATCTGCCGAACACACCTCGATTTGCAATACTACATT	365 GGCGGCGCGTCCTGGACGACACACACGCGCGCGTTGACATCTCTG  127 GlyvalArgValArgLeuLeuTleAspGlnLeuSerAlaIleSerAspLeuAsnIleLeu  425 CTGGCCCTCACAGCCATCCCAATATCGAAGGCCTGTTCACCCCTTCGTCCTA  11	Db 147 GlyAlaieuAlaGlyAlaHisValAsnPheGlnLeuArgIleTyrAsnProilePheGly 166  Qy 482 CGCAAATGGCGCGCACTCGGCTAC	Db 185 ArgPheAsnGlnArgMetHisA8nLysLeuLeuVallleAspGluMetlleGlyValVal 204 Oy 581 GGCGGACGCAATATCGGCGACGAGAGCCGCGGGGGGGGGCGCGCGC	225 ArgAspValLeuValAlaGlyProAlaValLeuGlnMetAlaValAsnPheAspAlaPhe 701 TGGGCAAGCCATTCCGCCCACACGCCACGCGCATCATCCGCAGCGGAACATCGGCAAG [		47

A; Fitle: The human MUCZ integrial mucin has cysteine-rich subdomains located both upstr A; Fitle: The human MUCZ integrial mucin has cysteine-rich subdomains located both upstr A; Restates not compared with conceptual translation A; Molecula type: mRNA A; Residues: 626-8195 < 6202- A; Corss-references: UNIPARC:UP100016AB12, GB:M94131; NID:g186395; PIDN:AAA59163.1; PID: A; Rocatelle type: mRNA A; Molecule type: mRNA A; Rocasion: 437300 < 6303- A; Rocasion: 437300 < 6303- A; Rocasion: 437300 < 6303- A; Rocasion: 437300 < 6303- A; Rocasion: 437300 < 6303- A; Rocasion: 437300 < 6303- A; Rocasion: 437300 < 6303- A; Rocasion: 437300 < 6303- A; Rocasion: 437300 < 6303- A; Rocasion: 437300 < 6303- A; Rocasion: 437300 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 43730 < 6303- A; Rocasion: 4770- A; Rocasion: 4770- A; Rocasion: 4770- A; Rocasion: 4770- A; Rocasion: 4770- A; Rocasion: 4770- A; Rocasion: 4770- A; Rocasion: 4770- A; Rocasion: 4770- A; Rocasion: 4770- A; Rocasion: 4770- A;	119 1248 1267 1267 1287 1287 1397 1317 1317 1317 1317 1317 1317
A;Title: Human bronchus and intestine express the same mucin gene. A;Reference number: A61257; MUID:91086481; PMID:1985113 A;Reference number: A61257; MUID:91086481; PMID:1985113 A;Reference number: A61257; MUID:91086481; PMID:1985113 A;Reference number: A61257; MUID:91086481; PMID:1985113 A;Rocaule type: mRNA A;Residues: YT',1925-1948, YTS',1952-1954 A;Residues: TY',1925-1948, YTS',1952-1954 A;Reprimental source: bronchus B;Au, G'; Human, L; Kharti, I'; Sajian, U.S.; MCCool, D.; Wang, D.; Jones, C.; Forstner, B;Arcession: PO0328 B;Au, G'; Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-thangerence number: P00328; MUID:92198477; PMID:1550588 A;Molecule type: mRNA A;Residues: 2328-2468 AXUG> A;Korss-references: UNIPARC:UP10000177AE2; GB:M86523 A;Molecule type: protein A;Cross-references: UNIPARC:UP10000177AE3 C;Genetics: C;Genetics: C;Genetics: C;Superfamily: von Willebrand factor type C repeat homology C;Reywords: glycoprotein; intestine; tandem repeat C;Reywords: glycoprotein; intestine; tandem repeat F;2766-2834/Domain: von Willebrand factor type C repeat homology C;Reywords: glycoprotein; intestine; tandem repeat F;2766-2834/Domain: von Willebrand factor type C repeat homology Pred. No.: B;200	Db 1387 nCysCysTrpProMetAspLysCysIleThrThrProSerProProThrThrThrThrProSe  401 ACGCGCGGGTTGGACGATCTCCTGCTCGCCCTCGACGCATCCCATATCGAAGTGCGC  Db 1407 rProProProThrThrThrThrThrThrThrThrThrThrThrThrThrT

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Db   751 OVAlThrSerSerThrThrGluSe	RESULT 15 G70063 G70063 C3Decies: Bacillus subtilis C;Becies: Bacillus subtilis C;Becession: G70063 C;Accession: G70063 R;Kunst, P.; Ogasawara, N.; Moszer, I. C; Bron, S.; Brouillet, S.; Bruschi, A.; Ehrlich, S.D.; Emmerson, P.T.; Ent Nature 390, 249-256, 1997 A;Authors: Foulger, D.; Fritz, C.; Fuj iech, J.; Harwood, C.R.; Henaut, A.; H	A; Authors: Lauber, J.; Lazarevic, V; Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, Rieger, M.; Rivolta, C.; Rocha, E.; R.; Ajuthors: Schleich, S.; Schroeter, R.; Ainters, P.; Wipet, A.; Yanamoto, A.; Authors: Yoshikawa, H.F.; Zumstein, A; Title: The complete genome sequence A; Reference number: A69580; MUID:98044 A; Accession: G70063 A; Status: preliminary; nucleic acid se A; Molecule type: DNA A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, A; Rocharder, THARSANDA, THARS	A;Experimental source: strain 168 C;Genetics: A;Gene: ywnE C;Superfamily: cardiolipin synthase C;Superfamily: cardiolipin synthase Alignment Scores: Pred. No.: Score: Sco	US-10-665-990A-13 (1-1561) x G70063 (1  Qy
	CCGACCTGGACATCCTCGCCACCGCGAGGTGTCGGCGAAGTATCGCACGACTTC	770 GCACTCGGATACAACGACGAAACA 793  544 rSerThrThrGluSerSerSerAlaProValProThrProSerSerSerThrThrGluSe 564  794 TCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACACGCCCCTCTACCAAAA 853  564 rSerSerThrProValThrSerSerThrThrGluSerSerSer-AlaProValProThrP 584  854 ATACAGACGGCGCTCTGGCAGAGCGTCCAAACCGCCTGATCAGCGACCC 910  558 ATACAGACGGCACGCATCGACAGAGCGTCCAAACCGCCTGATCAGCGACCC 910  558 ATACAGACGGCACGCATCGACAGAGCGTCCAAACCGCCCTGATCAGCGACCC 910  558 TCCTGCAAAAGGACTCGACGCGACCGCCAAACCGCCGCATTGCCGGGAGGCTGCAAGAC 910  511 CCTGCAAAAAGGACTCGACCGCGAACCGCCGAACCGCCGAATTGCCGGAGGCTGCAAGAC 970  512 CCTGCAAAAAGGACTCGACCGCCGAACCGCCGAACCGCCGAATTGCCGGAGGCTGCAAAAC 970  513 CCTGCAAAAAGGACTCGACCGCCCAAAACCGCCGCAATTGCCGGAGGCTGCAAGAC 970	604 hrGluSerSerAlaProAlaProThrProSerSerThrThrGluSerSerA 624 971 GCGCTCAAACAGCCCGAAAAAGCGTCTATCTGGTTTCACCCTACAAA 1030 624 laProValThrSerSerThrThrGluSerSerAlaProValProThrProSerSer 643 1031 TCCGGCACAGACGCACAAACTGGTGCAGGACGCATAGACGTTACCGTCCTGACC 1090 644 SerThrThrGluSerSerSerAlaProValProThrProSerSerSerThrThr 661 1091 AACTCGCTACAGGCGACCGACGCCGCCGC	TCGGCTACCTCAATACCGAAACCGCTCAAGCCGCATCAAACTCTAGG aProvalThrserserThrThrGluserSerSerAlaProvalThrserserThrThrGl -AGCTGCAACCCAACGCTCCCGCCACAAAGACAAGGCTCCCGGCATCAAAGACCAACCCACCATGCCTCCCCGCCACCAAAGACAAGGCCTGACGGCTCC -AGCTGCAACCCAACCTGCCCCCCCCCACAAAGACAAGGCCTCCCGGCACCCCCCCGGCACCTCCCCCCCC
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ntian, K.D.; Errington, J.; Fabret, C.; Ferrari, E
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A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.-
gh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinoi.
U.; Lee, S.M.; Levine, A.; Liu, H.; Mauda, S.; Maued
dega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecell
E.; Roche, B.; Rose, M.; Sadaie, Y.; Saro, T.; Scanlor
r, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serc
r, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyam
oto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
eln, E.; Yoshikawa, H.; Danchin, A.
ence of the Gram-Positive bacterium Bacillus subtilis
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                                                                                                                             ACCGCGTTACCCTCGACAACACAACC---GCCTGCAA 1453
                                                                                                                                                                                                                                                                                                                                                                          AAACCTACCCGAACGAAC -------CCGAA 1498
                                                                                                                                                                                                            | | | | :::
| SerSerThrThrGluSerSerValAlaProValProTh 811
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ThrSerSerAlaProSerSerThr 826
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::: pGluLeu 182	202 Qy 1499	517 215	CACCATA 577 F90001 16 hypothetical protein SA18 rGlyTyr 234 C;Species: Staphylococcue	GAGGAC 625	252	685 271	745	291	781 311	841	Alignment Scores: Pred. No.:	901	961	329 US-10-665-990A	Oy 134 TTCAMACTT   CTATTTCGTC 1021	341	1081 Db 140		CGTCAAA 1141 Db 15011: Db 15011: n1: n1: n2: n2: n2: n2: n2: n2: n2: n2: n2: n2	Oy 314		272 Qy 374	402 Db 187	1321 Qy	422 Db 200	Qy 494 GCACTCGGCT8 GAACAGAIG 1381 ::	442 0v 530	1441 Db 231
::: :::          :::          :::		458 CGCCTGTTCAACCCTTCGTCCTACGCAAATGGCGCGCACTCGGCTACCTGACCGACTTC :::	518 CCCGCCTCAACCGCCGCATGCACAAATCCTTTACCGCCGACAACCGCGCCACATA	CTCGGCGCACAATATCGGCGACGACTTC		626 ACCGTTTTCGCCGACCTGGACATCCTCGCCACCGCCAGCGTCGTCGGCGAAGTATCGCAC	686 GACTICGACCGCTACTGGGCAAGCCATICCGCCCACACGCCACGC	ArgPhelleLeuAspTrpAsnGln	746GCCAACATCGGCAAGGGTCTTCAAGACTCGGATAC  [     :::    292 HisPheProAspTyrGlyProLysGlyAsnValGlyMetGlnIleValThrSerGlyPro	782 AACGACGAAACATCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGTCGCCC	:::     312 AspSerGlu	842 CTCTACCAAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTGATC ::::::::   :::::    ::::	AGGGACACCCTGCAAAAGGACTGGACGGGGGGGGGGCGCGCAAACCGCCGA		962 CTGCAAGACGCGCTCAAACAGCCCCGAAAAAAGCGTCTATCTGGTTTTCACCCTATTTCGTC	330			1082 GTCCTGACCAACTCGCTACAGGGGACGACGTTGCCGCGTCCATTCCGGCTACGTCAAA					ACCTTCATTGTGGACGCAAACGCATCTTCATCGGCTCATTCA		1322 GCACGGCTCAATACCGGAAATGGGCGTCGTCATCGAAAGCCCCAAAATCGCAGAACAGATG	423 PheArgLeuAsnPheGluValAsnAlaPhelleTyrAspIleThrileAlaLysLysLeu	1382 GAGGGACCCTCGCCGATACCACACCGGAATACGCCTACCGCGTTACCCTCGACAAACAC
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Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc, R. Kobayashi, N.; Sawano, T.; Inoue, R.; Katro, C.; Sekimizu, K.; M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                     PROT:Q99SG9; UNIPARC:UP100000D778F; GB:BA000018; PID:G13701883; F
strain N315
                            PATGGCACGATCCCGCCACCCGAAA---ACCTACCCGAACGAACCCGAA 1498
                                               ::: |||||| ||||||| ::: ValSerArgLysPheThrTyrGluGluTyrLeuGln 463
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-----LysGlu 448
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                                                                                                                                                                                                                                                                                                                     equencing of meticillin-resistant Stapylococcus aureus. 758; MUID:21311952; PMID:11418146
                                                                                                                                                                                        1891 [imported] - Staphylococcus aureus (strain N315) us aureus
quence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                          TGGAAACGCATCGCCGCAAAATCCTATCCCTGCTG---CCCATC 1549
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112
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arst, U.  52, 2001  J.; Kuhn, M.; Kunst, F.; Kurapkat, G.  T.; Simoes, N.; Tierrez, A.; Vazque ve genomics of Listeria species.  AB1077; MUD:21537279; PMID:116796  Ary NA  GGLA>  : UNIPROT:Q92FU5; UNIPARC:UPI00000CC rce: strain Clipl1262  diolipin synthase  3.84e-10  Matches:	Conservative: 76	Oy 266 GAATCTGCCGAACACTTTGCAATACTACATTTGGCGCAACGACTTTCGGC 325  Oy 266 GAATCTGCCGAACACTCGATTTGCAATACTTTGGCGCAACGACTTTCGGC 325  153 ArgLysAlaGluAsnHisIleHisIleGlnTyrTyrIlePheLysThrAspAlaIleSer 172  Oy 326 AGGCTGCTGTTCAACCTTGCCGCAGAACGCGGCTGCGCTACGCTGCTG  173 ThrGluIleArgAspIleLeuvalGluLysAlaLysSerGlyvalGluValArgPheWet 192  Oy 386 TTGGACCAACACACGCGGGGTTCCTGCTGCTCGCTGCCTTGCACACACCTGCAACGCGCTGCTGCTGTTCAACACACAC	Oy 566 CGCGCCATACTCGGCGACGCAATATCGGCGACGAATAC
	327 327 340 340 342 365 365 365 365 375 375	Oy 1145 CGAAAACCGCTGCTCAAAGCCGGCATCAACTCTACGAGCTGCAACCCAACCATGCCTC 1204  Db 393 AlaAlaSerLeuLeuAspAlaGlyValLysValPheHisTyr	476 SULT 17 1433 1433 Species: Lis Species: Lis Caccession: A Glaser, P.; Dominguez-B

	GlyAspGluTrpAla 324	CTCTACCAAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTGATC 901	AGCGACACCCCTGCAAAAGGACTCGACCGCCGCAAACCGCCGATTGCCGGGAGG 961  Percent Similarity: 41.3%	ArgaspSer		CCTACAAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGACGCATAGACGTTACC 1	ProAspGludluAlaLeuAlaVallleArgArgValAlaMetSerGlyValAspValArg 381  Qy 177 GTCCTGACCAACTGGTAGCGACGGACGTTGCGGCTACGTACG	VD 4.7 S ValilelleProGlyLysGlyAspArgGlyIleSerPheHisGlySerAsnAla 399 Ov 216 -	TACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCATGCC 1201	TyrValLysThrMetIleGluAlaGlyAlaLysMetTyrAlaTyrAlaAspAspSerPhe 419  Qy 261 GTCCCGCCACAAAAGACAAAGGCCTGACCGGCAGCTCCGTAACCAGCTGCATGCCAAA 1261		ACCTICATIGIGGACGCAAACGCAICTICAICGGCTCAITCAACTICGACCCCGGITCC 13	AlaMetLeuValAspGlyThrArgAlaAlaIleGlyThrAlaAsnPheAspValArgSer 443  Qy 381 TGCTGTTGGACGACAACAACACGGGGGGGGGGGGGGGGG	GCACGGGTCAATACCGAAATGGGCGTGGTCGTCAAAATGGCCCCAAAATGGCAGAAGTG 1381	OY 441 ATCCCAATATCGAAGTGCGCCTTCAACCCTTCGACAACAC 1441	LeuHisLeuLysArgAspPheLysLysAspPhe	AACCGCCTGCAATGGCACGATCCCGCCACCGAAAAACCTACCCGAACGAA	File III Metaly saspinetes and manages and and and and and and and and and and	501 Qy 588	Db 162 ValSerValGlnProSerSerSerSerAlaProTl	Hent, pig) -Feb-1997 #text_change 09-Jul-2004	u-Cladaras, M.; Specian, R.D.; LaMont, J.T.	Gastroenterology 106, 200, 1994 A; Tille: Pig gastrio misology 106, 200, 1994 A; Reference number: 147141; MIDO:94102478; PMID:7506218 Db 202 SerSerValProThrThrSerThrThrSerValGlnP	/EMBL/DDBJ Qy 738	RC:UPI0000086746; EMBL:UI0281; NID:g915205; PID Db 222
300	320	Qy 842 CTCT. Db 325	902	Db 339 ArgA	342	Qy 1022 CCTA	Db 362 ProA Qy 1082 GTCC	0b 382 Vali	1142	Db 400 TyrV. Qy 1202 GTCC	420	Qy 1262 ACCT	424	Oy 1322 GCAC DD 444 PheA	QY 1382 GAGG	Db 462 LeuH	Qy 1442 AACO		۵	RESULT 18 147141	gastric mucin (clo C;Species: Sus scr C;Date: 21-Feb-199	C; Accession: 14714 R; Turner, B.S.; Bh	Gastroenterology 1 A;Title: Pig gastr A;Reference number	A; Accession: 14714 A; Status: prelimin	A;Molecule type: m A;Residues: 1-528 A:Cross-references

81; NID: 9915205; PIDN: AAC48526.1; PID: ones encoding pig gastric mucin. 55593 GCGAAGTATCGCACGACTTCG--- 692
:::|||:::|||
:ValSerValGlnThrSerSer 201 -----AGGACACCGTTTTCG 635 CCGCCCACACGCCACGCGCATCA 737 |||| :::::: ProSerSerSerSerValPro 221 TCG-----GATACA 782 |||| |SerSerThrProlleProSerThr 241 ----TGGACAACATCCTGCAAA 176 ACAACGGGCTATCCGACATCT--- 215 AAGCCCTTGCCGCCCGCCCCCCCCC ACTACATTTGGCGCAACGACATTT 320 CAGAACGCGCGTGCGCGTACGCC 380 ATCTCCTGCTCGCCTCGACAGCC 440 ::: ||| |||:::::: valGlnSerSerSerSerSer 107 TCCTACGCAAATGGCGCGCACTCG 500 |||| |Ser-----Ser 121 TGCACAACAAATCCTTTACCGCCG 560 ThrThrSerAlaThrSerValGln 181 ACGCGCTCCTGCGCTACCGCGAAA 824 :::||||||| ThrSerSerSerSerProPro 61 |||| :::::::: ||ThrSerSerSerSerVal 76 SerSerSerSerAla---- 92 ThrThrSerThrThrSerValGln 21 |||::: |ThrSerValGlnProSerSerSer 41 .. ..

qq	::: :::	A;Cross A;Exper	A;Cross-references: UNIPROT:039781; UNIPARC:UPI00000ECBA1; EMBL:D88733; PIDN:BAA20037.1 A;Experimental source: strain HH1
Qy	825 CCGTCGAACAGTCGCCCCTCTACCAAAAATACAGACGGACGCATCG 872         :::    262 ProSerSerSerSerThrProlleProSerThrThrSerValGlnProSerSerSer	C;Genet A;Note: C;Super F;558-8	C;Genetics: Abote: ORF71 C;Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein hor F;558-866/Domain: equine herpesvirus 1 glycoprotein homology <ehg></ehg>
<i>&amp;</i> 8	873 ACTGGCAGAGCGTCCAAACCCGCCTGATCAGCGACCCCCTGCAAAAGGACTCGACCGCG 932 :::	Alignme Pred. N Score:	Alignment Scores: 5.6e-10 Length: 866 Score: 297.50 Marches: 122
ð i	ACCGCCGCAAACCGCCGATTGCCGGGAGGCTGCAAGACGCGCTCAAACAGCCCGAAAAAA 9	Percent Best Lo Query M	Percent Similarity: 39.2% Conservative: 72 Best Local Similarity: 24.6% Mismatches: 222 Query Match: 10.4% Indels: 79
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q	328 SerSerGlySerAlabrothrThrSerAlaThrSerValGlnProSerSerSerSerSer 347	8	246 CCGCCCGCGCCCTTATCGAATCTGCCGAACACCCTCGATTTGCAATACTACATTT 305
	GAAAACGCTGCTCAAAGCGCTCGCTCA	Д	
g à	348 ProProlieSerSerInrileSerValGinProSerSerSerSerSerSerProThrThr 367	ð i	GGCGCAACGACATTTCCGGCAGCTGCTGTTCAACCTCATGTACCTTGCCGCAGAACGCG
	11/3 ANCIETACGAGGIGCAAACCAAACCAAGCGGCGCGCGCGCGGGGCGTGGGCGTGGGGGCGTGGGGGG	a è	75 SerThrSerThrGinSerSerSerSerThrAlaAlaThrSerSerSerAlaProSerThrAla 94
	GCAGCTCCGTAACCAGCCTGCATGCCAAAACCTTCATTGTGGACGGCAAACGCATCTTCA	<b>3</b> 6	
οp	:::   :::     388 ValGlnProSerSerSerSerSerValProThrThrSerAlaThrSer 403	ò	TCGCCCTCGACATCCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCTACGCA
λŏ	1293TCGGCTCATTCAACCTCGACCGCTCCGACGGCTCAATACCGAAATGGGGG 1346	QQ	
엄	404 ValArgSerSerSerSerThrProlleProThrThrThrSerValGlnProSer 423	ò	486 AATGGCGCACTCGGCTACCTGACCGACTTCCCCCGCCTCAACGCGCGCATGCAACA S45
	TCGTCATCGAAAGCCCCAAAATCGCAGAACAGATGGAGCGCACCC	Ор	127
		δλ	546 AATCCTTACCGCCGACAACCGCCACCATACTCGGCGGACGCAATATCGGCGACGAAT 605
	TGGCGGATACCA	q	139AlaAlaSerThrAlaAlaSerThrSerAlaGluThrThrThrAlaThrAla 155
	ThrProlleProSerThrThrSerValGlnProSerSerSerSerSerAlaProThrThr 46	À.	ACTICAAAGICGGIGAAGACACCGITITCGCCGACCIGGACAICCTCGCCACCGGCAGCG
à a	1437 AMCHALMACCCIGCTAMIGGCACGACCCGCACCCGGAAAAACCTTACCCGAACG 1490 :::    :::    :::    :::	a è	156 ThrAlaThrSerThrFroThrThrThrThrProThrSerThrThrThrThrThrThrAlaThr 175 666 Thompseansalathrangsanangsanangsanangsanangsanangsanangsanangsanangsanangsanangsanangsanangsanangsanangsana
ŏ	AACCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAATCC 1532	G QQ	ThrThrValProThrThrAlaSerThrThrThrAspThrThrAhalaAlaThrThr 19
ΩÞ	::: :::   ::: 483 SerValGlnProSerSerSerSerSerProThrThrSer 496	ò	726 CCACGCGCATCATCCGCAGCGCGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACG 785
RESULT 19 T45462		qq	
membrane C;Species	glycoprotein (imported] - equine herpesvirus 1 : equine herpesvirus 1	ζ	786 ACGAAACAICCAGACACGCGTCCTGCGCTACCGCGAAACCGTCGAACAGTCGCCCTCT 845
C;Date: 3 C;Accession	1-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004 on: T45462	Db	215 ThralaalaThrThralaalaThrThrThrAlaalaThrThrThrAlaalaThrThr 234
R, Kirisaw J. Equine	,	λo.	846 ACCAAAAAAATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTGATCAGCG 905
A;Tltle: A;Referen	Nucleotide sequences of open reading frames 1, 24 and 71 of an attenuated equince number: 222973	q	
A; Accessi A; Status: A; Molecul A; Residue	A;Accession: T45462 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-866 <kir></kir>	که و	906 ACACCCCTGCAAAAGGACTCGACCGCGACGGCGAAACCGCGGATTGCCGGGGGGGCTGC 965 

Oy 966 AAGACGCGCTCAAACAGCCCGAAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCTA 1025		
::: :::     ::: CAL ThrThrThrThrThrAlaAlaThrThrAlaAlaThrThrThrAlaAla 291	ò	126 GCCGTCAT    :::
Qy 1026 CAAAATCCGGGACAGACGCACTGGCAAAACTGGTGCAGGGGATAGAGGTTACCGTCC 1085	q ў	19 AlaileG
	δ'n i	
Qy 1086 TGACCAACTCGCTACAGGCGACCGACGTTGCCGCCGTCCATTCCGGCTACGTCAAATACC 1145	α <u>α</u> •	
	λ i	246 CCGCCCG
Qy 1146 GAAAACCGCTGCTCAAAGCCGGCATCAACGTCTACGAGCTGCAACCAAC	qq (	
Db 326 AlaThrThrGlySerProThrSerGlySerThrSerThrThrGlyAlaSerThrSer 345	<u>.</u>	306 GGCGCAA
Qy 1206 CCGCCACAAAAGACAAAGGCTGACCTGACCGCAGCTCCGTAACCTGCCTG	g ;	
Db 346 ThrProSerAlaSerThrAlaThrSerAlaThrPro357	S &	
Qy 1266 TCATIGTGGACGCAAACGCATCTTCATCGGCTCATTCAACCTCGACCCCCGTTCCGCAC 1325	- A	426 TCGCCCTC
Db 358ThrSerThrSerThrSerAlaAlaAlaThrThrSerThrProThrProThr 374	G 40	
1326 GGCTCAATACCGAAATGGGGGTCGTCATCGAAAGCCCCAAAATCGCAGAACAGATGGAGC :::	ò	
375 SerAlaAlaThrSerAlaGluSerThrThrGluAlaProThrSerThr	QQ	112 ThrProT
1386 GCACCCTCGCCGATACCACACGAATACGCCTACCGCGTTACCCTCGACAAACACAACC	ò	540 ACAACAA
391ProThrThrAspThrThrProSerGluAlaThrThr	qq	 132 ThrThrT
1446 GCCTGCAATGGCACGATCCCGCACCGAAAAACCTAC	ò	600 ACGAATA
404 AlaThrThrSerProGluSerThrThrValSerAlaSerThrThrSer	ব্য	   150 ThrAlaT
1485	۵	660 GCAGCGT
	ପ୍	 170 AlaThrT
1515GCATCGCCGCAAAAATCCTATCCTGCTGCCCATCG	ò	720 ACAACGC
Db 440 ThrSerThrAlaGluProSerSerThrPheThrLeuThrProSer 454	දිය	<del> </del> 189 ThrThrTl
RESULT 20 T45463	ò	780 ACAACGA
membrane glycoprotein [imported] - equine herpesvirus 1 C;Species: equine herpesvirus 1	qa	 209 ThrThrT
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004 C;Accession: T45463	ò	840 CCCTCTA
•	qa	229 ThrThrT
nuated	equin Qy	900 TCAGCGA
A;Accession: 145463 A;Status: preliminary; translated from GB/EMBL/DDBJ	qa	249 ThrThrTl
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		954 CCGGGAG
1: BAAZUU38	dO Db	269 ThrThrA
n rotein	VQ OY	1014 ATTTCGT
	qq	289 ThrThrA
Length:	δλ	1074 ACGTTAC
t Similarity: 38.7%	ପ୍	303 ThrThrT
10.3% Indels:	ò	1134 ACGTCAA
	qu	323 ThrThrT
US-10-665-990A-13 (1-1561) X 145463 (1-867)	_	

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rcctacaaaatccggcacagacgcactggcaaaactggtgcaggacggcatag 1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCA 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3GCTGCAAGACGCGCTCAAACAGCCCCGAAAAAGCGTCTATCTGGTTTTCACCCT 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isalaThrThrAlaAlaThr------ThrThrAlaAla 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ThrAlaAlaThrThrThrGlySerProThrSerGlySerThrSerThrThrGly 342
VITTCAATACTTCCAAACCTGTCCTCGACAACATCCTGCAAATCCGGCACA 185
                                                                                                           ATAACAACGGGCTATCCGACATCTACCTGCTCGACGACCCCCACGAAGCCCTTG 245
                                                                                                                                                                                                                                                                                                                            ACGACATITCCGGCAGGCTGCTGTTCAACCTCATGTACCTTGCCGCAGAACGCG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                  SCGTACGCCTGCTGGTGGACGACAACAACACGCGGGGGTTGGACGATCTCCTGC 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rccacaccarcccaararccaagrccccrcrrcraccccrrrccraccca 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::|||::|||||||
| hrThrSerIleProThrSer-----ThrSerThrGluThrThrThr 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3CGCACTCGGCTACCTGACCG-----ACTTCCCCCGCCTCAACCGCCGCATGC 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThralaSerThrThrThrProThrThrThrThrAlaAlaProThrThrAlaAla 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCTTTACCGCCGACAACCGCGCCACCATACTCGGCGGACGCAATATCGGCG 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTICAAAGICGGIGAGACACCGIITIICGCCGACCIGGACAICCICGCCACCG 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rcsrcaccaagtarcacaccaccaccaccacracracrasscaagccarrccaccc 719
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ThrThrValPro---ThrThrAlaSerThrThrThrAspThrThrThrAlaAla 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACGCGCATCATCCGCAGCGGCAACATCGGCAAGGGTCTTCAAGCACTCGGAT 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGAMACATCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGTCGC 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCADADADATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTGA 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACACCCTGCAAAAGGACTCGACCGCGACCGCGCA----AACCGCCGATTG 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThralaalaThrThrSerSeralaThrThralaAlaThrThrThrAlaAlaThr 268
                                                                                                                                                                                                                    SCGCCGCCCTTATCGAATCTGCCGAACACACGCCTCGATTTGCAATACTACATTT 305
                                    94
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|ThrAlaAlaThrThrAlaAlaThrThrAlaAlaThrThrAlaAla
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221 CTCGACGACCCCCACGAAGCCCTTGCCGCCCCCCCTTATCCAATCTGCCGAACAC 280 138 learnhandsonglyglud	
6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B	6 6 6 6 6
1199 ACCATGCCGTCCGGCGACAAAGGCAGACGGCGGCGGCGCGCGC	Qy 41 AAAACAGGCAGCCTCATTTATGCCTCTCTGTTCATGGTTG 100

	Db 263 GyvyslavalryzhladerClinThaAggPhelleMetApTrpAsnESer 282  0y 797 AGACCCCCCCCCTCCCCTACCCCAAACCCCCC 841  Db 283 ThHHSISEAEPTyLySALACTYCCCCCCAACCCCCC 841  0y 103 SerNeCCTCLACAAAACCCCCCCCCCCCCCCCCCCCCCCCCCCC
Qy         1277 GGGAAAGGCTCATTCAACCTCGACCCCCGTCCGACGGCTCAATACC 1336           Db         429 GlythrArgalaalalaIleGlyThrAlaAsnPheAspValArgSerPheArgLeuAsnHis 448           Qy         1337 GAAATGGGCGTCCTCATCGAAAGCCCCAAAATGCGAACAGATGGACCCCTCCCC 1396           A49 GluLeuMetValPheLeuTyrAspGluSerGluAlaMetHisHisLeuLysArg 466           Qy         1397 GATACCACCCCGAATACGCCTACCGCGTTACCCTCGACAACACACAC	RESULT 22 A17022 A17022 A17022 A17022 A17022 A17024 A17022 A17025 C.58pecies infocus C.58

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AG1387 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst. U.	Oy 842 CTCTACCAAAAATACAGACGGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTG 898     ::: :::      ::: Db serMetGln1leValSerSerGlyProAspSerGluTrpGlnGln1leLysAsnGlyTyr 322
ence 294, 849-852, 2001 withors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma C.; Schludter, T.; Simoes, M.; Tierre, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,	Qy 899 ATCAGCGACACCCTGCAAAAGACTCGACCGCGACCGCCGAAACCGCCGATTGCCGGG 958
Reference number: ABIO77; MUID:21537279; PMID:11679669	959 AGGCTGCAAGACGCGCTCAAACAGCGACGTCTATCTGGTTTTCACCCTATTTC
Molecule type: DNA Residues: 1-482 <gla> COSS-references: UNIPROT:Q8Y4B3; UNIPARC:UPI0000055715; GB:NC_003210; PIDN:CAD00581.1 Experimental course: etrain FGD-a</gla>	325MetlleAsnAlaAlaLysLysThrIleTyrLeuGlnSerProTyrPhe 3 1019 GTCCTACAAAATCCGGCACAGACGCACTGGCAAAACTGGCAGAGGCGCATAGACGTT 1 :::    :::
Genetics: Gene: lmo2503 Superfamily: cardiolipin synthase	341
2.21e-09 Length: 287.00 Matches:	Db 361 ArgValMetIleProAsnLysProAspHisAlaPheValTyrArgAlaThrThr 378 Qy 1139 AAATACCGAAAACCGCTGCTCAAGCCGGCATCAACTCTACGAGCTGCAACCCAACCAT 1198
Percent Similarity: 39.0% Conservative: 57  Best Local Similarity: 25.5% Mismatches: 164  Query Match: 10.1% Indels: 164  Conc. 10.1% Indels: 164	Db 379 AsnřýrAlaGlyGluLeuMetGluThrGlýAlaLýsIlePhe 392 Qy 1199 GCCGTCCCGCCACAAAAGACAAAAGGCTCAGCCGGCAGCTCCGTAACCAGCCTGCATGCC 1258
-10-665-990A-13 (1-1561) x AG1387 (1-482)	
OY 206 TCCGACATCTACCTGGACGACCCCGAGGAGCCCTTGCCGCCCGC	Qy 1259 AAAACCTTCATTGTGGACGGCAAACGCATCTTCATCGGCTCATTCAACCTCGACCCCGT 1318  402 LysThrLeuValValAspGlyGluIleAlaSerValGlyThrAlaAsnMetAspPheArg 421
266 GAATCTGCCGAACACACCTCGATTTGCAATACTACATTTGGCGCAACGACATTTCGGC 32	Qy 1319 TCCGCACGCTCAATACCGAAATGGCGTCGTCAAAGCCCCCAAAATCGCAGAACAG 1378
326 AGGCTGCTGTTCAACCTCATGTACCTTGCCGCAGAACGCGGCGCGCGC	Qy 1379 ATGGAGCGCACCTCGCCGATACCACACCCGAATAC 1414
386	Oy 1415 GCCTACGC 1423 
446 AATATCGAAGTGGGCCTGTTCAACCCCTTGGTCCTAGGCGAAATGGCGGCGCTCGGCTAC 5	RESULT 24 T45025 TWOIN WUCSB, tracheobronchial (imported) - human (fragment)
506 CTGACCGACTTCCCCGCCTCACCGCAGCGCAGCAACAAATCCTTTACCGCCGACAACAACAACAAATCTTACGCCGACAACAACAACAACAAAATAAAAAACAACAACAAAAAAAA	C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T45025 T;Besseyn, J.L.; Guyonnet-Duperat, V.; Porchet, N.; Aubert, J.P.; Laine, A. J. Biol. Chem. 272, 3168-3178, 1997
566 CGCGCCACATACTCGGCGACGCAATATCGGCGAATACTTCAAAGTGGTGAGGAC 62 231 AspValGlyTvt11eGlyGlyPheAsn11eGlyAsnGl)HTVI-ndlyAlaser 24	A;Title: Human mucin gene MUCSB, the 10.7 kb large central exon encodes various alterna A;Reference number: 222899; MUID:97166151; PMID:9013550 A;Accession: T49025 A;Accession: T49025
626 ACCGTTTTCGCCGACCTGGACATCCTCGCCACCGGCAGCGTCGTCGGCGAAGTATCGCAC 68	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-3570 <pre>cDES&gt; A; Cross-references: UNIPARC:UPI000016AD88; EMBL:272496; NID:q1834502; PIDN:CAA96577.1;</pre>
Db 249 LysLysPheGly 252	
OY 746 GGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGAAACATCC 796	t Similarity: 21.7\$ Mismatches:
Oy 797 AGACACGCGCTCCTGCGCTACCGGAAACCGTCGAACAGTCGCCC 841	Query Match: 10.0% Indels: 282 DB: Gaps: 27 US-10-665-990A-13 (1-1561) x T45025 (1-3570)

1014 ATTTCGTCCTACAAAATCCGGCACAGACGCACTGGCAAAACTGG 2208 IleThrThrValValThrThrGlyCysGluProGlnCysAlaTrpSerGluTrpLeuAsp 1058	Qy         1118		Db 2467 ValalaThrProSerSerThrProGlyThrÄläHisThrThrLysValbroThrThrThr 2486  Qy 1317
Oy 141 CTTCCAAACCTGTCCTGGACAACATCCGGCAACCCCTCATAACA 197 1868 LeuProAlaLeuArgSerThrAlaThrThrProThrAlaThrSer 1882 Oy 198ACGGGCTATCCGACATCTACCTGCThrProThrAlaThrSer 1882 Oy 198ACGGGCTATCCGACATCTACCTGCTCGACG 227 1983 ValThrAlaIleProSerSerSerLeuGlyThrAlaTrpThrArgLeuSerGlnThrThr 1902 Oy 228 ACCCCACGAAGCCTTGCCGCGCCGCCGCTATCGAATCTGCCGAAC 278 1903 ThrProThrAlaThrMetSerThrAlaThrProSerSerThrProGluThrValHis 1921 Oy 279 ACGCCTCGATTGCAATACTACATTGGCGCAACGACATTTCCGGCAGCTGCTTCTA 338	Qy         339 ACCTCATGTAGCGGAACGCGGCGTGCGGTACGCCTGTTGGACGAACA 398           1940 ThrProSerSerThrProGlyThrAlaHisThrThrLysValProThrThr 1956           Qy         399 ACAGGCGGGTTGGACGATCTCCTGCTCGCCCTCGACAGCCATC	Oy 561 ACAACCGCCCACATACTCGGCGGACGAATATCGGCGAACGAA	TACGGGAAACGGTGAAC

15)   Db   312 ValLysTyrPheProLysLysAsnGlyProLeuGly	DD 362 OY 1073 OY 1133 OY 1133 OY 1133 DD 400 OY 1193 160 DD 416	1253 CATGCCAAACCTTCATTGTGGACGCAAACGCATCTTCATCGGCT	232  RESULT 26  562  H867LT 26  H867LT 26  H867LT 26  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  C, Species: Lac  A, Title: The  A, Title: The  A, Title: The  A, Status: prel  A, Status: prel  A, Status: prel  A, Molecule typ  A, Status: prel  A, Status: prel  C, Genetics: Lac  C, Con
G89906 hypothetical protein SA1155 [imported] - Staphylococcus aureus (strain N3 C; Species: Staphylococcus aureus C; Species: Staphylococcus aureus C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-20 C; Accession: G89906 E; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I. ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; C.; Shhab, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus au A; Reference number: A89758; MUID:21311952; PMID:11418146 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-505 ckUR> A; Experimental source: strain N315 C; Genetics: A; Genetics: A; Garatise SA1155 C; Superfamily: cardiolipin synthase	1.1e-09   Length: 505     284.50   Marches: 103     284.50   Marches: 103     38.3	GCCTTATCGAATCTGCCGAACACAGCCTCGA 	Phe

Alignment Scores	Db 351 LeuAlaLeuLeuSerGly	1112	369	Qy 1172 AAACTCTAGAGCTGCAA	Db 389 Lysvalryr	Qy 1232 GGCAGCTCCGTAACCAGC	CCGC 253 Db 398	aleu 134   Ov 1	313	154 00 412	373 QY 1352	174 Db 432	424 Oy 1412	4 4 4	484 Qy 1472	457 LeuGluArgT	517 CIATCO	Sn 214 Db 477	RESULT 3	234	634	254	ICGAC 694 A.Aceference number: A83650; MUID	e 274	754	A;Experimental source: str.	IGCGC 814 A;Gene: A Gene A	Couperramenty carcifornian 311 cannot consort.	CATC 871 Pred. No.:	s 300 Percent Similarity: Rest Local Similarity:	C 931 Query Match:	-665-990A-13 (1-156	991 Qy 167	330	1051 Qy 218	, ,
### Scores:  # 4.06e-09 282.50  ### Similarity: 39.04 39.04 39.04 39.04 39.04 39.04 39.04 39.04 39.04 30.04						(1-481)	TACCTGCTCGACGACCCCCACGAAGCCCTTGCCGC	LysIlePheAsnAspGlyArgGlnLysPheAsnAl	GAACACACCCTCGATTTGCAATACTACATTTGGCC	:::     ::: ::::          :::   LysHisHisValHisMetGluTyrTyrIlePheA:	TTCAACCTCATGTACCTTGCCGCAGAACGCGGGGG	::::::::::::::::::::::::::::::::::::::	GACAACACACGCGGGTTGGACGATCTCCTG	::: TrpGlySerAsnLysThrLys	AATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCT	:::::: GlubeuGln	:CTGACCGACTTC	::: .valAlaGlnPhePheProLeuIleMetProLeuVa	CACAACAATCCTTTACCGCCGACAACCGCGCCA(	  HisArgLysIleValValIleAspGlyIleIleG	GACGAATACTTCAAAGTCGGTGAGGACACCGI	  AspGluTyrAlaSerIleThrLysLysPheGlyT		ThrelyAspileValTyrSerLeuGlnHisArgP	GCCCACAACGCCACGCGTCATCCGCAGCGGCA		GGATACAACGACGAAACATCCAGACGCGCTCC7	AsnSerGlnHis	TCGCCCCTTACCAAAAATACAGACGGACGCATC	GluProTyrPheProAspSerileValGluGlyH	CGCCTGATCAGCGACACCCCTGCAAAAGGACTCG	GlnLeuValThrSerGlyPro	GCCGGGAGGCTGCAAGACGCGCTCAAACAGCCCGJ	:LysLeuThrTyrMetLysMetIleSerGlyAlaG		ory Ily Ileriose Asparaheunisciuse Il
	110		ı.		١ ،	_	AACAA	rĠiy	9000	IleAs			GTACG	:: 5 Vally			5 AAATG		0000	F ProAr	CTCGG	5 ThrG	s gccgA	ArgAs	CGCTA	5 LeuAs	s ggcaa	00	TACCG	HisPh	GACTG		GACCG	AspGl	AGCGT	Tinis

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taki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
11, 2000
nce of the alkaliphilic bacterium Bacillus halodurans and
1D:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (8Z4; UNIPARC:UPI0000127B9A; GB:AP001516; GB:BA000004; NII
-125
                                         CGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCATC 1171
                                                                                                                         ACCCAACCATGCCGTCCCGCCACAAAGACAAAGGCCTGACC 1231
                                                                                                                                                                                                        CCTGCATGCCAAAACCTTCATTGTGGACGGCAAACGCATCTTC 1291
                                                                                                                                                                                                                                                                                            CGACCCCCGTTCCGCACGGCTCAATACCGAAATGGGCGTCGTC 1351
                                                                                                                                                                                                                                                                                                                                                                           CGCAGAACAGATGGAGCGCACCCTCGCCGATACCACCCCGAA 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCGACAAACACACGCCTGCAATGGCACGATCCCGCCACC 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAACCCGAAGCCAAACTTTGGAAACGCATCGCCGCAAAAATC 1531
                                                                   pAlaThrTyrPheHisAlaAlaAspLeuValLysTyrGlyAla 388
                                                                                                                                                 ||| ::: |||
----ThrTyrGluAsnGlyPhe--- 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | |||||| :::|||| sargLeualaasnAsnProlleSerPheSerThrAsnThrLys 143
yValGlnValLysLeuLeuIleProAsn-----LysProAsp 368
                                                                                                                                                                                                                                  .::||||:::|||||||
-ValHisSerLysThrLeulleIleAspGlyGluTyrAlaSer 411
                                                                                                                                                                                                                                                                                                                    CACCCTCATAACAACGGGCTATCC-----GACATCTAC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAAGCCCTTGCCGCCCGCCCCTTATCGAATCTGCCGAA 277
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sdluThrPheAlaHisIleLysGlnAlaLeuArgMetAlaThr 163
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Db 449 GluValAsnAlaPheLeuTyrArgTh	Qy 1397 GATACCACACCGAATACGCCTACCGGTTACCCTCGACAAACACACCCTCGTCTCACAAACACACCCTCTCTCACAAACACACAC	Qy 1457 CACGATCCCGCCACCCGAAAAACCTAC 1483 	RESULT 28 C04125 cardiolipin synthetase BH3803 [imported] - Bacillus halodurans (stre C;Species: Bacillus halodurans	C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-J C;Accession: C84125 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui Nucleic Acids Res. 28, 4317-4331, 2000	A/fitle: Complete genome sequence of the alkaliphilic bacterium Baci A/Reference number: A83650; MUID:20512582; PMID:11058132 A/Accession: C84125 A/Status: preliminary	A;Nolecule type: DNA A;Residues: 1-398 SYSTO> A;Cross-references: UNIPROT:09K6C6; UNIPARC:UPI0000C42DC; GB:AP0015 A;Experimental source: strain C-125	Cjenetics: AjGene: BH3803 CjSuperfamily: cardiolipin synthase	1.1e-08 Length: 275.00 Matches:	Percent Similarity: 37.9% Conservative: 63  Best Local Similarity: 23.9% Mismatches: 172  Query Match: 9.6% Indels: 108  DR. 108	-10-665-990A-13 (1-1561) x C84125 (1-398)	Qy 179 CGGCACCCCTCATAACAACGGGCTATCCGACATCTACCTGCTCGACGACCCC	239 GCCTTGCCGCCGCGCGCCCTTATCG		Db 73 TyrilePheArgAspAspHisIleGlyLysLysIleLeuGlnHisLeuGluGln Qy 359 GAACGCGCGCGCGCTGCCTGCTGGACGACAACAAC	Db 93 LysGluGlyValAlaValArgLeuLeuValAspArgPheGlyAlaAspValLys  Qy 407 GGGTTGGACGATCTCCTGCTCGCCTCGACAGCCATCCCAATATCGAAGTGCGC	Db 113 SerIleGlnSerLeuLysGlnAlaGlyAlaGlnPheGluTyrAlaHisArg  Qy 467 AACCCTTGTCCTACGCAATGGCGCGCACTCGGCTACCTGACCGACTTCCCC	Db 132 PheProTyrTrp	Db 140 AsnArgArgAsnHisArgLysIleThrVallleAspGlyLysIleGlyTyrIle Oy 587 CGCAATATCGGCGACGAATACTTCAAAGTCGGTGAGGACACCGTT	Db 160 TyrksniledlykspóluTyrLeudlykrgksperoLysLeuGlyPhe Qy 638 GACCTGGACATCCTCGCCACCGGCAGCGTCGTCGGCGAAGTATCGCACGACTTC
:::     :::	338 AACCTCATGTACCTTGCGGAGAACGCGGGGGGGGGCTGCTGCTGGTTGGACGACAAC 397 184 GlulleLeumetGlnLysAlaLysGluGlyIleHisValArqPheLeuTyrAsDGlyVal 203	CCATCCCAATATCGAAGTG :::   ::: sGlnAlaGlyValGlulle	458 CGCCTGTTCAACCCCTTCGTCCTAGGAATGGCGGGGCACTCGGCTACCTGACCGACTTC 517	518 CCGCGCCTCAACCGCCGCATGCAACAAATCCTTTACCGCCGACAAC 565	566 CGCGCCACCATACTCGGCGAATATCGGCGACGAATACTTCAAAGTCGGTGAGGAC 625 :::	626 ACCGTTTTCGCCGACCTGGACATCCTCGCCACCGGCAGCGTCGTCGGCGAA 676	677 GTATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAACGCCACGCGCATC 736 :::	ATCCGCAGCGGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGAAGAACATCC	303	304	LeuThrasnMetLysAspAspGlyGlyValGlnMetlleAlaSerGlyPro	917 AAAGGACTCGCGACCGCGCAACCGCCGATTGCCGGGAGGCTGCAAGACGCGCTC 976	977 AAACAGCCGAAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCCTACAAAATCCGGC 1036 :::      ::::::::		1097 CTACAGGCGACCGTTGCCGCGTTCCGGCTACGTCAATACCGAAAACCGCTG 1156			1277 GGCAAACGCATCTTCATCGACTCGACCCCCGTTCCGCAGGCTCAAAACC 1336 	
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C;Species: Clostridium perfringens
C;Species: Clostridium perfringens
C;Accession: T43863
R;Koyama, M.
Submitted to the EMBL Data Library, August 1998
A;Description: Clostridium perfringens hem operon.
A;Reference number: Z22707
A;Accession: T43863
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-476 <KOX>
                                                                                                                                                                                                                                                                                                                                                  TACTGGGCAAGCCATTCCGCCCACACGCCACGCGCATCATCCGCAGCGCCAACATCGGC
                                                                                                 AAGGGTCTTCAAGCACTCGGATACAACGACGAAACATCCAGACACGCGCTCCTGCGCTAC
                                                                                                                                                         CGCGAAACCGTCGAACAGTCGCCCCTCTACCAAAAATACAGACGGGACGCATCGACTGG
                                                                                                                                                                                                                 878 CAGAGCGTCCAAACCCGCCTGATCAGCGACACCCCTGCAAAAGGACTCGACCGCGACCGC
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A,Cross-references: UNIPROT:Q9ZNC6; UNIPARC:UPI000016E0DF; EMBL:AB017186; PIDN:BAA74786. A;Experimental source: strain NCTC8237; vegetative cell cyfenetics: A;Genetics: A;Genetics: C;Superfamily: cardiolipin synthase
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|AsnlleSerLeuLysTyrLysAspLeuIleMetAsnPheAsnAsnAspAsnSerThr 105
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Tyr-----LeuGlyLysAspLys-------
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Percent Similarity: 40.4% Conservative: 56 Best Local Similarity: 27.3% Mismatches: 162 Query Match: 9.5% Indels: 93 DB: 2 Gaps: 18 US-10-665-990A-13 (1-1561) x H82711 (1-467)	Oy 218 CTGCTCGACGACGCCCTGCCGCGCCGCGCCCCTAATCGAATCTGCCGAA 277	Oy 278 CACAGCCTCGATTTGCAATACTACATTTGGCGCAACGACGCTGCTGTTC 337 :::	Qy 338 AACCTCATGTACCTTGCCGCAGAACGCGGCGTGCGGGTGCTGCTGTTGGACGAC 394 :::	Oy 395 AACAACACGCGGGGTTGGACGATCTCCTGCTCGACCACCACCATCCCAATATCGAA 454	7 :	Qy 515 TTCCCCGGCTCAACCGCGGATGCAACAAATCCTTTACCGCGGACAACGGCGCCACC 574	Oy 575 ATACTCGGCGGACGAATATCGGCGACGAATACTTCAAAGTCGGTGAGGACACCGTTTTC 634	0.00   0.00	Qy 1160 AAAGCCGGCATCAAAACTCTACGAGCTGCCAACCATGCCGTCCCCGCCACAAAAGAC 1219
	OY 1019 GTCCTACAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGCGCATAGACGTT 1078	<pre>Qy 1079 ACCGTCCTGACCACTTGCTACAGGCGACCGACCGTTGCCGTCCATTCCGGCTACGTC 1138</pre>	Oy 1139AAATACCGAAAACCGCTGCTCAAAGCCGCATCAAACTCTACGAGCTGCAACCC 1192	Qy 1193 AACCATGCCGCCACAAAAGACAAAGGCCTGACGGGAGCTCGGTAACCAGCCTG 1252	Qy       1253 CATGCCAAAACCTTCATTGTGGACGCAACGCATCTTCATCGGCTCATTCAACCTCGAC 1312         Db       :::   :::            394 HisAlaLysThrIleValalaAspSerSerIleCysSerValGlyThrAlaAsnMetAsp 413	Qy 1313 CCCGTTCGCACGGCTCAATACCGAATGGGCGTCGTCATCGAAAGCCCCAAAATCGCA 1372	Qy 1373 GAACACATGGAG 1384 :::        Db 434 LysSerMetGlu 437	LT 30  iolipin synthase XF1209 [imported] - Xylella fastiocies: Xylella fastidiosa ecies: Xylella fastidiosa ete: 18-Aug-2000 #sequence_revision 20-Aug-2000 #tc cession: 182711-157, 2000  Lle: The genome sequence of the plant pathogen Xyl ference number: A82515; MUD: 20365717; PMID: 109103  te: for a complete list of authors see reference ression: H82711  atus: preliminary lecule type: DNA mpson, A.J.G.; Renlach, F.C.; Arruda, P.; Abreu, F. lecule type: DNA mpson, A.J.G.; Renlach, F.C.; Arruda, P.; Abreu, F. perimental source: strain 9a5c  number: AS9328  nument scores:  nument scores:	Pred. No.: 2.05e-08 Length: 467 Score: 270.50 Matches: 117

383  Qy 460 CCTGTTCAACCCCTTCGTCCTACGCAAATGGCGCGCACTCGGCTACCTGACCGACTTCCC	1339 Db 796 SerProLysProArgGiyLeuGinArgSerArgArgArgArgArgArgSerArgSerArgArgArgArgArgArgArgSerArgSerArgArgArgArgArgSerArgSerArgArgArgArgArgArgArgArgArgArgArgArgArg	433	1	Oy 814 CTACCGCGAAAACCGTCGACCGTCTACCA	Db   901 SerProAlaThrHisArgArgSerArgThrProLeulleSerArg	Db 938 Oy 1036 Db 953	1791   1791	231 ON 1195 CCATGCCGTCCCGCCACAAAAGACAAAAGGCCTGACCGGCAGCTCCGTAACCAGCTGCACTGCACTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGCTGCAGAAGACAAAAGACAAAAGACTGAAAAGACAAAAAGACTGAAAAGACAAAAAAAA	282 1255 TGCTATATGTGGGGGAAAGCTTCATTGTGGCTCTTCATGTGGCTCATTCAT	746 Db 1036 399 Db 1054 766 Oy 1375	1439
371 ArgAlaGlylleLyslleAlaLeuTyrArgProHisPhe	AAACGCATCTTCATCGATCGACCCGATCCGATCCGATCC	IleGlyMetIleCysTyrAspSerArgIleValSerArgLeuArgGluValGluSerAsp   ACCACACCCGAATACGCTTACCCTCGACAAACACACGCCTGCAATGCAC 	GATCCCGCCACCCGAAAAACC 1480            :::::: GlnArgProAlaTrpArgArgSer 455	T02345  hypothetical protein KIAA0324 - human (fragment)  C;Species: Homo sapiens (man)  C;Date: 05-Mar-1999 #text_change (C;Accession: T02345  C;Accession: T02345  R;Ricke, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunt et, J.; White, S.; Hong, S.; Tatum, O.; Cambbell, C.; Fawcett, Te, Reille, Reil	submitted to the EMBL Data Library, March 1998 A;Description: Sequencing of human chromosome 16p13.3. A;Reference number: 214664 A;Accession: T02345 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1791 < RIC. A;Cross-references: UNIPROT:060382; UNIPARC:UP100000730AE;	C;Genetics: A;Map position: 16 A;Introns: 1610/2; 1706/2 A;Note: KIAA0324	Arigument Scores: Prid Marches: Score	US-10-665-990A-13 (1-1561) x T02345 (1-1791)  OY	ccacgaagcccttgccgcccgcgccgcccttatcgaatctgccgaacacag    ::::::		CACGCGGGGTTGGACGATCTCCTGCTCGCCCTCGACAGCCATCCCAATATCGAAGTGCG

Db 244 CysGlyPheValGlyGlyHisAsnValGlyValGluTyrLeuGlyGluLysPro 261 Qy 629 GTTTTGGCGACCTGGACATCCTGGCCAGGGAGGGGGGGAAGTA 679	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	1034 1034 354 1094 374	1154 392 392 1214 407 1274 415 1394 415 1394 425 SULT 33 0089 rddolipin 8) 806089 rddolipin 8) 71118 815 82 80 J. 14, 58 8
	RESULT 32 B82371 Cardiolipin synthase PA5394 [imported] - Pseudomonas aeruginosa (strain PAO1) Cardiolipin synthase PA5394 [imported] - Pseudomonas aeruginosa C;Species - Rseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C;Accession: B82971 R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathot A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Reference preliminary A;Accession: B82971 A;Accession: B82971 A;Accession: B02971 A;Accession: B02072 A;Cession: B02073 A;Accession: B02073	2.88e-08 268.00 37.7% ity: 24.5%	US-10-665-990A-13 (1-1561) x BB2971 (1-490)  Oy  95 TGGTTGCCCCATGGAAGAACGGAAGCCGTCATTTCAATACTTCCAAACCTGC 154  Db  97 TPATGPLOTTPUT

Wed May

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1118 GCCGTCCATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTC 1177
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ThrAlaAsnMetAspMetArgSerPheGInLeuAsnPheGluValAsnValPhePheThr 452
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                                                                        ------LysTyrGlyPhePheAsnGln-----LysLeuAsnPheArgAsnHis
                                                                                                                     542 AACAAATCCTTTACCGCCGACAACCGCGCCACCATACTCGGCGACGCAATATCGGCGAC
                                                                                                                                                               243 ArgiysileValileIleAspGlyLysThrGlyPheValGlyGlyLeuAsnValGlyLys
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C,Species: equine herpesvirus 1
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
R;Glaser, P.; Danchin, A.
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R;Glaser, P.; Danchin, A.
R;Glaser, P.; Danchin, A.
R;Description: Cloning and sequencing of the Bacillus subtilis chromosomal region from 3
A;Reseduce submer: S55414
A;Accession: S5544
A;Accession: S5544
A;Accession: S5544
A;Accession: S5544
A;Residue; 142-200 < GLAA
A;Cross-references: UNIPARC;UPIO00016E83F; EMBL:Z49782; NID;8653752; PIDM:CAA8961.1; PI
R;Kunst, F.; Ogaawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brucoullet, S.; Brusoni, C.; Carter, N.M.; Cinc
A; Ehrlich, S.D.; Emmerson, P. (C.); Endita, M.; Pujita, Y.; Fuma, S.; Galizzi, A.; Galler
R;Kunst, F.; Ogaawara, N.; Moszer, I.; Albertini, A. M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.D.; Emmerson, P. (C.); Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
N; Richors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Layine, Y.; Sato, T.; Scanlon, A;Authors: Lauber, J.; Lazarevic, V.; Lee, B.; Rose, M.; Sadoie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schreeter, R.; Scoffone, F.; Scoffone, F.; Scoffone, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schreeter, R.; Scoffone, F.; Scoffone, Y.; Sato, T.; Minters, Yoshikawa, H.; Danchin, A.; Toasto, V.; Uchlysma, A;Atchors: Voshikawa, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Toasto, V.; Manamoto, H.; Yamanoto, H.; Yamanoto, H.; Vasumoto, K.; Yata, K.; Yata, K.; Accession: F70059
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|131 AlaHisMetAsnIleAsnThrLysSerAsnIleLysValLeuLysAsnGlyGluGluThr
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A,Note: host Equus caballus (domestic horse) C.Date: 30-Sep-192 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004	ò	551 TTTACCGCCGACAACCGCGCCACCATACTCGGCGGACGAATATCGGCGACGAATACTTC 610
R,Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.	DÞ	197 aAlaThrThrAlaAlaThrThrThrThrAlaAlaThrThrAlaAlaThrThrAlaAlaThrThrThrAl
submitted to GenBank, March 1992 A; Description: The DNA sequence of equine herpesvirus-1.	ò	AAAGTCGGTGAGGACACCGTTTTCGCCGACCTGGACATCCTCGCCACCGGCAGCGTCGTC
A; Accession: H36802 A; MOlecule type: DNA	qa	:
A;Residues: 1-797 <tel> A;Cross-references: UNIPROT:P28968; UNIPARC:UPI0000138750; GB:M86664; NID:g330791; PIDN:</tel>	ò	671 GGCGAAGTATCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACAAGGCCACG 730
	q	227 rAlaThrThrAlaAlaThrThrThrAlaAlaThrThrThrAl 241
A;Title: The DNA sequence of equine herpesvirus-1. A;Reference number: A41831; MUID:92295566; PMID:1318606 A;Contents: annotation; possible protein-coding frames A;Nore: neither amino acid nor muclactide commence is diven	ò a	731 CGCATCATCCGCACCACCACCACCAAGGCTCTTCAAGCACTCGGATACAACGACGA 790
C,Genetics: A,Gene: 71 C,Superfamily: equine herpesvirus glycoprotein X; equine herpesvirus 1 glycoprotein homo	දු දු	791 ACATCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGTGGCCCCTTACCAA 850
C;Keywords: glycoprotein; transmembrane protein F;1-22/Domain: signal sequence #status predicted <sig> F;23-797/Product: qlycoprotein X #status predicted <mat></mat></sig>	ò	ACACC
F;23-465/Region: serine/threonine-rich F;489-797/Domain: equine herpesvirus 1 glycoprotein homology <ehg></ehg>	qa	280
F;766-790/Domain: transmembrane #status predicted <tmn> F;590/Binding site: carbohydrate (Asn) (covalent) #status predicted</tmn>	ර ස	911 CCTGCAAAAGGACTCGACCGCGCGCGAACCGCCGATTGCCGGGAGGCTGCAAGAC 970
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OY 431 CTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCTACGCAAATGG 490  :::	6 G	rThrGluAlaLeuGluThrProAspGlyAsnThrThrSerGlyAsnThrThrProSerPr
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ò	616 CGGTGAGGACACCGTTTTCGCCGACCTGGACATCCTCGCCACCGGCAGCGTCGGCGA 675	.; Lor Nature	Lory, S.; Ole ture 406, 959-
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۸۵	796 CAGACACGCGCTCCTGCGCGAAACCGTCGAACAGTCGCCCCTCTACCAAAAAT 855	c; suber	ramily
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	ογ	916 AAA	AGGACTCC	PACCGCGACC	GCCGCAAACCGCCGATT	AAAAGGACTCGACCGCGGCGCAAACCGCCGATTGCCGGGAGGCTGCAAGACGCGCT	975
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	٥٨	976 CAA	ACAGCCCC	SAAAAAGCG	TCTATCTGGTTTCACCC	CAAACAGCCCGAAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCTACAAAATCCGG	1035
	QQ	356	-LysAlaT	hrLysTyrVa	alTyrileThrThrPro	.:: LysAlaThrLysTyrValTyrIleThrThrProTyrLeuVallleGlyAsnGluMe	374
	δ	1036 CAC	AGACGCAC	TGGCAAAACT	rggtgcaggacggcata	CACAGACGCACTGGCAAAACTGGTGCAGGGCATAGACGTTACCGTCCTGACCAACTC	1095
	qq	374 tVa	lThrAlai	euThrSerA]	laAlaLysGlyGlyVal.	tValThrAlaLeuThrSerAlaAlaLysGlyGlyValAspValArglleIleThrProHi	394
	ζ	1096 GCT	ACAGGCGA	CCGACGTTGC	CCCCCTCCATTCCGCC	GCTACAGGCGACGTTGCCGCCGTCCATTCCGGCTACGTCAAATACCGAAAAACCGCT	1155
	qq	394 sile.	-	roAspLysLy		-ProAspLysLysIleValHisSerValThrLysSerTyrTyrLysValLe	412
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	ò	1336 CGAJ	AATGGGCG	TCGTCATCGA	AAAGCCCCAAAATCGCA	CGAAATGGGGGTCGTCGAAAAGCCCCAAAATCGCAGAACAGATGGAGGGCACCCTCGC	1395
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	ờ	1456 GCAC	CGATCCCG	CCACCGAAA	VAACCTACCCGAACGAA	GCACGATCCCGCCACCCGAAAAACCTACCCGAACGAACCGGAAGCCAAACTTTGGAAACG	1515
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λō	263 ATCGAATCTGCCGAACACAGCCTCGATTTGCAATACTACATTTGCCGCAACGACATTTCC 322	286
q	5 ilegluhlahladinArgSerileGlubeuGlubeuTyrLeuValGluAspGlyHisCys 24	1364
ò	323 GGCAGGCTGCTTCAACCTCATGTACCTTGCCGCAGACGCGGCGTACGCCTG 382	1001
qq	25 AlaGluLeuPheLeuValAlaLeuLeuAspAlaArgArgArgGlyValAlaValArgCys 44	000
ò	383 CTGTTGGACGACAACAACACGCGGGGTTGGACGATCTCCTGCTCGCCCTCGACAGCCAT 442	ABSOLI SO AH2333
qq	 45 LeuPheAspGlyPheGlyCysLeuGlySerAlaTrpIleGlnArgLeuArgGlu 64	Calulolipin synchase tampo C;Species: Nostoc sp. PCC
λŏ	443 CCCAATATGGAAGTGGGGCTGTTTGAACCCCTTCGTCCTACGCAAATGGCGCGCACTCGGC 502	C)Date: 14-Dec-2001 #seque
qa	65 AlaGlyGlyGlyGluLeuArgLeuTyrAsnProLeuArgTrpLysLeuThrGly 81	C. Accession: A42333 R. Kaneko, T.; Nakamura, Y.
δ	S03TACCTGACCGACTTCCCCCGCCTCAACCGCATGCAATCCTTT 553	Nakazaki, N.; Shimpo, S.; DNA Res. 8, 205-213, 2001
QQ	82 GlyAsnLeuTyr	A; Reference number: AB1807
ò	554 ACCGCGGCAACCGCGCCACCATACTCGGCGGACGCAATATCGGCGACGAATACTTCAAA 613	Acception: Aircol
qa	93 LeuValAspGlyArgLeuGlyTyrValGlyGlyAlaGlyIleThrAspGluPheTrpGlu 112	A; MOIECUIE LYPE: DNA A; Residues: 1-480 «KUR>
ò	614GTCGGTGAGGACACCGTTTTCGCCGGACCTGGACATCCTCGCCACCGCACGTCGTC 670	A:Experimental source: str
qq	113 ProvalSerAspvalSerAlaTrpArgGluvalMetValGluMetAspGlyProvalVal 132	A; Sunerfamily. cardiolinin
ογ	671 GGGGAAGTATCGCACGACGCTACTGGGCAAGCCATTCCGCCCACACGCC 727	Alignment Scores.
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ò	728ACGCGCATCATCCGCAGCGCAACATCGGCAAGGGT 763	
qq	153 LysProArgGluGlyMetThrLeuThrArgLeuProProGlnProGlyAlaAlaAlaAgGly 172	Desc Docal Similaricy: 23 Query Match: 9.
δλ	764 CTTCAAGCACTCGGATACAACGACGAACATCCAGACACGCGCTCCTGCGCTACCGCGAA 823	35-13 (1-156
οp	173 LeuGlyArgValAlaTyrAlaAsp180	THE TO BE
ò	824 ACCGTCGAACAGTCGCCCCTCTACCAAAAATACAGACGGACG	
qq	181Ala 181	-
ò	CCCTGCAAAAGGACT	701
QQ	182 ArgGlnHisArgAspIleLeuGlnSerLeuValArgAlaLeuAsnGlySerArgArg 201	0 0
ò	944 CCGCCGATTGCCGGGAGGCTGCAAGACGCGCTCAAACAGCCCCGAAAAAAAGGCGTCTATCTG 1003	601
Db	202IleTrpLeu 204	7 7 7
ò	1004 GITTCACCCTATTTCGTCCCTACAAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAG 1063	
QQ		1 C
ò	1064 GACGGCATAGACGTTACCGTCTGACCAACTCGCTACAGGCGACGGACG	329 CIGCIGIICAAC
q	225 ArgGlyvalGluvalArgLeuLeuLeuAlaGlyArgLeuThrAspHisAlaProval 243	380
ò	1124 CATTCCGGCTACGTCAAATACCGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAG 1183	181
QQ	244 ArgTyrAlaGlyGlnArgTyrTyrProArgLeuLeuArgAlaGlyValArgIleHisGlu 263	449
δò	CTGCAACCCAACCATGCCGTCCCCGCCACAAAAGACAAAAGGCCTGACCGGCAGCTCCGTA	201
q	264 TyrGlnProArgPhe 268	Qy 509 ACCGACTTCCCC
δ	1244 ACCAGCCTGCATGCCAAAACCTTCATTGTGGACGGCAAACGCATCTTCATCGGCTCATTC 1303	

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.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S'
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana. 77; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCT: QBYPH1; UNIPARC: UPI0000CEA63; GB: BA000019; PIDN: BAB75922.1; rain PCC 7120
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:7120
: PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
ence_revision 14-Dec-2001 #text_change 09-Jul-2004
                                                               CCGTTCCGCACGCTCAATACCGAAATGGGCGTCGTCATCGAAAGCCCC 1363
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aGluAlaPheIleGlyIleProPheThrSerGlyAsnAsnAla----- 122
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Wed May

QQ	217GlnLeuAsnPheArdAsnHisArdLysIleLeuValValAsnGlyArg 232	N.Alternate names.
è	できた。	C.Species: Homo sapiens ("
	ThralaPhelleGlyGlyLvanaralleSerAspGlufyrLeuGlyLysAsnPro	C,Accession: T43481; T3454 R;Koehrer, K.; Bever, A.;
'n		submitted to the Frotein; A:Reference number: 22251
Dp 5		A; Accession: T43481 A; Molecule type: mRNA
δy	680 TCGCACGACTTCGACCGCTACTGGGCAAGCCATTCCGCCCACACGCCACGC	A;Residues: 1-580 <aaa> A;Cross-references: UNIPRC</aaa>
Dp 7	271 GlnGlyCysPheLeuGlnAspTrpTyrTrpAlaThr 282	A, Experimental source: adu R, Poustka, A.; Wellenreuth
0y	734 ATCATCCGCAGCGCAACATCGGCAAGGGTCTTCAAGCACTCGGATACAACGACGAAACA 793	submitted to the Protein S A:Reference number: Z21540
Dp 7	282 283	A; Accession: T34549 A: Molecule rype: mRNA
ζ.	794 TCCAGACACGCGCTCCTGCGCTACCGCGAAACCGTCGAACAGTCGCCCCTCTACCAAAAA 833	A; Residues: 262-580 APOUL)
Db 2		A;Experimental source: adu R;Poustka, A.; Klein, M.;
o <sub>y</sub>	854 ATACAGACGGACGCATCGACTGGCAGAGCGTCCAAACCCGCCTGATCAGCGACACC 910	submitted to the Protein S A; Reference number: Z18723
Dp 5		A;Accession: T17264 A;Molecule type: mRNA
6 YO	911 CCTGCAAAAGGACTCGACCGCGACCGCGAAACCGCCGATTGCCGGGAGGCTG 964	A; Residues: 262-580 < POU2> A; Cross-references: UNIPAR
Db 3	 309 ProAlaAspLysLeuLysAlaCysLysLeuPhePhe 320	A, Experimental source: adu C, Genetics:
Oy 9	965 CAAGACGCGCTCAAACAGCCCGAAAAAAGCGTCTATCTGGTTTCACCCTATTTCGTCCCT 1024	A;Note: DKFZp434C196.1; DF
Dp 3		Alignment Scores: Pred. No.:
Oy 10	1025 ACAAAATCCGGCACAGACGCACTGGCAAAACTGGTGCAGGACGGCATAGACGTTACCGTC 1084	
	341 AspAspSerThrLeuThrAlaLeuLysLeuAlaAlaLeuArgGlyValAspValArglle 360	Best Local Similarity: 27 Query Match: 8.
0, 10	1085 CTGACCAACTCGCTACAGGCGACGTTGCCGCGTCCATTCCGGCTAACGTCAAATAC 1144	
	:::	US-10-665-990A-13 (1-1561)
Qy 11	1145 CGAAAACCGCTGCTCAAAGCCGGCATCAAACTCTACGAGCTGCAACCCAACCATGCCGTC 1204	Qy 154 CCTCCTGGACAA
	379 TyrThrGluMetLysAlaThrAsnIleLysLeuTyrArdTyrLysHisGlyPhe 396	Db 82 ProProArgAla
•	1205 CCCACADABAGACABABAGACABABAGACABAACABAACA	Qy 196 CAACGGCTATC
		Db 102 AlaSerProThr
	THE CALLES OF CALLES AND CHARACTER OF THE CALLES OF CALL	Qy 246
ξ, 4 4		Db 122 ProMetArgThr
		Qy 294 AATACTACATTT
	PheLeuAsnPheGluValMetGlvPheValAlaAsnSerGlnPheValIvsSerValGlu	Db 142 GlyThrProSer
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	AACCGCTGCAATGGCAACGATCCCGCAAAAAACCGGAAACGAAAAAACCAAAAAAAA	Qy 405 GCGGGTTGGACG
	460 GluArg	Db 174 aSerLeuThrAr
00	1543	Qy 456 TGCGCCTGTTCA
l	TyrLeuTrpPheLysLeuAlaValArglleSerSerLeuLeu	Db 194 oThrArgThrPr
RESULT 39		Qy 516 TCCCCGCTCA
T43481 probable mu	T43481 probable mucin DKFZp434C196.1 - human (fragment)	Db 214 rProProArgAl

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ROT:09UF83; UNIPARC:UPI00006D400; EMBL:AL133561; NID:g6599133, dult testis; clone DKFZp434C196 ther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. Sequence Database, October 1999
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AARC:UPI0000070F36; EMBL:AL122069; NID:g6102864; PIDN:CAB59245.2
dult testis; clone DKFZp434B0635; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
i Mewes, H.W.; Gassenhuber, 1.; Wiemann, S.
i Sequence Database, September 1999
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ARC:UPI0000070F36; EMBL:AL117481; NID:g5911958; PIDN:CAB55954.1
dult testis; clone DKFZp434B061
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Sequence Database, December 1999
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NALernate names: DNA-directed RNA polymerase B largest chain

C, Species: Homo sapiens (man)

C, Species: Homo sapiens (man)

C, Species: Homo sapiens (man)

C, Species: Homo sapiens (man)

C, Species: Homo sapiens (man)

C, Accession: S21054; S18987

R, Mintreatth, M.; Acker, U.; Vicaire, S.; Vigneron, M.; Kedinger, C.

R, Mintreatth, M.; Acker, U.; Vicaire, S.; Vigneron, M.; Kedinger, C.

R, Title: Complete sequence of the human RNA polymerase II largest subunit.

A, Reference number: S21054; MUID: 92178992; PMID: 1542581

A, Roelecule type: mRNA

A, Roelecule type: mRNA

A, Rosiduces: 1-1790 cMIN>

A, Rosiduces: 1-1790 cMIN>

C, Genetics:

A, Gene: GDB: POLRAA; POLRA

A, Cross-references: GDB: 120306; OMIM: 180660

A, Map position: 17p13.1-17p13.1

C, Superfamily: human DNA directed RNA polymerase II largest chain

C, Superfamily: human DNA directed RNA polymerase II largest chain

C, Superfamily: human DNA directed RNA polymerase; tandem repeat; transcription; zinc finger F;71-87/Region: zinc finger CCHH motif |||||||||| ::: ||| ||| ||| SerProSerTyrSerProThrSerProSerTyrSer 1630 (671 TyrserProThrserProSerTyr---SerProThrserProSerTyrSerProThrSer 1689 |||| |----AlaThrProAlaTyrGlyAlaTrpSerPro 1533 1554 AlaSerGlyPheSerProGlyTyrSerProAlaTrpSerProThrProGlySerProGly 1573 ServalGlySerGlyMetThrProGlyAlaAlaGlyPheSerProSerAlaAlaSerAsp 1553 CCGGCAGCGTCG-----TCGGCGAAGTATCGCACGACTTCGACCGCTACTGGGCAAGCC 710 TGGAAGAACGGACGGAAAGCCGTCATTTCAATACTTCCAAACCTGTCCTCCTGGACAACA 167 CCGCCCGCCCCCTTATCGAATCTGCCGAACACACCCTCGATTTGCAATACTACATTT 305 GCGTGCGCGTACGCCTGCTGGTTGGACGACAACACGCGCGGGGTTGGACGATCTCCTGC ----AATGGCGCGCACTCGGCTACCTGACCGACT---TCCCCCCCCCTCAACCGCCGCA GCGACGAATACTTCAAAGTCGGTGAGGACACCGTTTTCGCCGACCTGGACATCCTCGCCA GGCGCAACGACATTTCCGGCAGGCTGCTGTTCAACCTCATGTACCTTGCCGCAGAACGCG TCGCCCTCGACAGCCATCCCAATATCGAAGTGCGCCTGTTCAACCCCTTCGTCCTACGCA TGCACAACAAATCCTTTACCGCCGACAACGCGCCACCATACTCGGCGGACGCAATATCG TCCTGCAAATCCGGCACACCCCTCATAACAACGGGCTATCCGACATCTACCTGC-----1970 123 69 196 115 SerProGlyProSerSerProTyrIleProSer------Length:
Matches:
Conservative:
Mismatches:
Indels: 657 ò

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Search completed: May 2, 2006, 05:26:35 Job time : 143 secs

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version 5.1.7 - 2006 Biocceleration Ltd.
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GenCore
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OM protein

May 2, 2006, 06:09:35 ; Search time 41 Seconds (without alignments) 1232.044 Million cell updates/sec Run on:

US-10-665-990A-14 2720 1 MHTDPKIQAMPSETISPMKT......KLWKRIAAKILSLLPIEGLL 525 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues

Searched:

283416

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 1: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

phopholipase D-fam cardiolipin synthe probable synthase probable synthase conserved hypothet hypothetical 55.9K phospholipase D fa conserved hypothet probable cardiolip conserved hypothet cardiolipin syntha Description SUMMARIES B81859 B81883 B81083 B81083 B90806 B95656 G97556 G97556 G97556 G97003 F70003 F7 H86744 B84007 C84125 T43863 H82711 B82971 S60089 AE3539 D83103 E97307 Query Match Length DB 5555 5656 5666 2.00022 2.00022 2.00022 2.00002 2.00002 2.0 2643 2573 1102.5 1100.5 1093.5 1089.5 Score о В Result 

cardiolipin syntha	cardiolipin syntha	cardiolipin synthe	cardiolipin synthe	probable phospholi	cardiolipin syntha	cardiolipin syntha	cardiolipin syntha	probable phospholi	ybhO protein - Esc	probable synthetas	cardiolipin synthe	cardiolipin synthe	cardiolipin syntha	cardiolipin synthe	cardiolipin syntha
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	.5	11.5	235	228	26.5	24.5	224.5	224	221	221	221	219	219	217	216
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## ALIGNMENTS

	y protein NMA1646 [imported] meningitidis	d) - Neisseria meningitidis (strain 22491
	C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 C;Accession: B81859	2000
		K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mores. S.: Moule, S.: Mundall, K.: Onail, M. B.: Balandream
	Nature 404, 502-506, 2000	
	A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491 A;Reference number: A81775; MUID:20222556; PMID:10761919	A strain of Neisseria menigitidis 22491. D:10761919
	A; Accession: B81859	
	A;scarus: preliminary A;Molecule type: DNA	
_	tal source: serogroup A,	UNIFAKC:UF1UUUUUSUSSF; GB:ALI627S6; GB:ALI57S59; NI strain 22491
	C;Genetics: A;Gene: NMA1646	
	cardiolipin synthas	
	Query Match 97.2%; Score 2643; DB 2; 1 Best Local Similarity 97.3%; Pred. No. 5.2e-182; Matches 511. Concervative 5. Micmatches 9.	DB 2; Length 525; 2e-182; Tidale 0. Gang 0.
	QY 1 MHTDPKIQAMPSETISPWKTRSLISLICLLICGCSSWLPPLEERTESRHFWTSKPVLLDN	SCSSWLPPLEERTESRHFNTSKPVLLDN 60
	Db 1 MRANPKTQAMPSETISLAKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVRLDN	SCSSWLPPLEERTESRHFNTSKPVRLDN 60
	Qy 61 ILQIRHTPHNNGLSDIYLLDDPHEALAARALIESAEHSLDLQYYIWRNDISGRLLFNLM	IESAEHSLDLQYYIWRNDISGRLLFNLM 120
	Db 61 ILQIRHTPHTNGLSDIYLLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLV	
	Qy 121 YLAAERGVRVRLLLDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRL	PNIEVRLFNPFVLRKWRALGYLTDFPRL 180
	Db 121 YLAAERGVRVRLLLDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRL	
	Oy 181 NRRWHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWA	OTVFADLDILATGSVVGEVSHDFDRYWA 240
	Db i81 NRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWA	
	Qy 241 SHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGKIDWQSV	ALLRYRETVEQSPLYQKIQTGRIDWQSV 300
	Db 241 SHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSV	ALLRYRETVEGSPLYQKIQTGRIDWQSV 300

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                                                            ymdC protein - Escherichia coli (strain K-12)
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R'STettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Oin, H.; Vamathevan, J.; Salth, H.O.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Tille: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUID:2017575; PMID:10710307
A; Rocession: B81083
A; Retus: prediminary
A; Molecule type: DNA
A; Residues: 1-508 «TET->
A; Cross-references: UNIPROT:Q9JYU0; UNIPARC:UP10000C46E9; GB:AE002494; GB:AE002098; NIC
A; Experimental source: serogroup B, strain MC58
C; Genetics:
A; Gene NMBA434
C; Superfamily: cardiolipin synthase
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                                                                                                                     Score 2573; DB 2;
Pred. No. 5.2e-177;
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Matches 497; Conservative
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Conserved hypothetical protein STY1185 [imported] - Salmonella enterica subsp. enterica (5,5pecies: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies: Salmonella typhi (5,5pecies
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C;Genteics:
A;Genteics: GTY1185
C;Superfamily: cardiolipin synthase
                                                    305 ISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDV 364
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Best Local Similarity
Matches 221; Conserval
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C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D8566
R;Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Fitle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Recence number: A85480; MUD:21074935; PMID:11206551
A;Accession: D8566
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-493 <C3TO-
A;Cross-references: UNIPROT: Q8X917; UNIPARC:UPI0000165766; GB:AE005174; NID:g12514578; E
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Genetics:
                              Cross-references: UNIPROT:Q8X917; UNIPARC:UD100000D07ED; GB:BA000007; PIDN:BAB34847.1; 
Experimental source: strain 0157:H7, substrain RIMD 0509952
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.larity 47.4%; Pred. No. 3e-71;
Conservative 84; Mismatches 143;
A,Residues: 1-493 < HAY>
A,Cross-references: UNIPROT:Q8X917;
A,Experimental source: strain O157:FC;Genetics:
A,Gene: ECs1424
C,Superfamily: cardiolipin synthase
                                                                                                                                                                                                                                                 Similarity
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Best Local 8
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Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AB2777
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-518 <KUR>
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525
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Matches 204; Conservative
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G97556
hypothetical 55.9K protein in csgc-mdog intergenic region [imported] - Agrobacterium tum
C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Accession: G97556
K; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
R; Goodner, B.; Hinkle, G.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 1213-12129, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A; Reference number: A97159; MUID:21608551; PMID:11743194
A; Reference number: A97159; MUID:21608551; PMID:11743194
A; Residues: prelliminary
A; Molccule type: DNA
A; Residues: 1-518 «KUR»
A; Residues: 1-518 «KUR»
A; Residues: UNIPROT:Q8UEX3; UNIPARC:UPI0000DIC0B; GB:AE007869; PIDN:AAK87408.1;
C; Genetics:
A; Gene: AGR C 2007
A; Map position: circular chromosome
C; Superfamily: cardiolipin synthase
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DVIVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHA-VPATKDKGLTGSSVTS 421
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A,Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: E71963
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-502 <ARN>
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                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9ZMP2; UNIPARC:UP1000013942E; GB:AE001456; GB:AE001439; NI
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Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Y.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAOL, an opportunistic pathora. Reference number: A82950; MuID:20437337; PMID:10984043
A;Reference number: A82950; MuID:20437337; PMID:10984043
A;Reference number: Dreliminary
A;Residues: 1-529 cSTO
A;Cross-references: UNIPROT:O9HTP4; UNIPARC:UPI00000C5F9D; GB:AE004943; GB:AE004091; NID
A;Experimental source: strain PAOI
C;Genetics:
A;Gene: PA5310
C;Superfamily: cardiolipin synthase
conserved hypothetical protein PA5310 [imported] - Pseudomonas aeruginosa (strain PAO1)
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C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: E71963
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 LGNWLENLTWARAEAIWDAPLKVLSRGEPDPHLLLSPHLAGLFKGVQKELILVSAYFVPA 345
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                               Species: Pseudomonas aeruginosa
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRFLLLLALIALIALSGCASTPPPQPSSALPAEGTWLARQAE------IQGRDHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 HNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 HNAT----RIIRSGNIGKGLQALGYNDETSRHALLRY--RETVEQS----PLYQKIQTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 RPIEDFLWRAPYPGEL-------SSARRKLQRYLRKESVKESGYIRHLFDRGDQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---LEERTESRHFNTSKPVLLDNILQIRHTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86; Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 29.1%; Score 792; DB 2; Best Local Similarity 36.7%; Pred. No. 4.9e-49; Matches 200; Conservative 86; Mismatches 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 RSLISLLCLLLCSCSSWLPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521 IEGLL 525
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LEKML 529
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conserved hypothetical secreted protein HP0190 - Helicobacter pylori (strain 26695)
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                                                                                                                                                                                                                                                                                                                                     DISGRILFNLMYLAAERGVRVRLLLDDNNTRGLD----DLLLALDSHPNIEVRLFNPFVL 165
                                                                                                                                                                                                                                                                                                                                                                 RKWRALGY---LIDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 ATGSVVGEVSHDFDRYWASHSAHNATRIIRS------GNIGKGLQALGYNDETSRHAL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 LRYRETVEQSPLYQ-KIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 KDSVFIASSYFIPGKKIMKIFKNQISKGIELNILTNSLSSTDAIVVYGAWERYRNKLVRM 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :||: : | | :||| 315 GANVYEIRNDFFNRQIKGR---FSTKHSLHGKTIVFDDALTLLGSFNIDPRSAYINTESA 431
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                                                                                                                                                                                                                       64 IRHTPHNNGLSDIY-------LLDDPHEALAARAALIESAEHSLDLQYYIWRN
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                         26;
                                                                                                                   Length 502;
                                                                                                             Query Match 23.2%; Score 632; DB 2; Length 502 Best Local Similarity 32.8%; Pred. No. 1.4e-37; Matches 161; Conservative 93; Mismatches 181; Indels
C,Genetics:
A,Gene: jhp0176
C;Superfamily: cardiolipin synthase
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M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Reference number: A59328
                                                                                                                                                                                                                 Matches 161; Conservative
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                                                                                                                                                                                         Similarity
                                                  A; Contents: annotation C; Genetics:
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Best Local
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Cardiolipin synthase XF1087 (imported) - Xylella fastidiosa
Ccisecision: S82724
Cardiolipin synthase XF1087 (imported) - Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent R;anonymous, The Second Sequent S;anonymous, The Second Sequent Salary A;Reference number A59128 below
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59128 below
A;Residues DNA
A;Residues 1-652 cSIMA
A;Residues 1-652 cSIMA
A;Residues 1-652 cSIMA
A;Residues 1-652 cSIMA
A;Residues 1-652 cSIMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNL 441
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                                                                                                                                                                                                                                                                                   DISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLD----DLLLALDSHPNIEVRLFNPFVL
                                                                                                                                                                                                                                                                                                                                                                                                         RN-KGLRYFEMLADYERIKKRMHNKLFIVDNFAVIIGGRNIGDNYFDNDLDTNFLDLDAL
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                                                                                                                                                                                                                 RKWRALGY---LIDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 ATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVE
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                                                                                                                                              92;
                                                                                              23.1%; Score 627; DB 2; Length 502; larity 31.5%; Pred. No. 3.2e-37; Conservative 86; Mismatches 161; Indels
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DPRSAYINTESAVLFDNPSFAKRV----
  C;Genetics:
A;Start codon: TTG
C;Superfamily: cardiolipin synthase
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                                                                                           Query Match
Best Local Similarity
Matches 156; Conserv
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cardiolipin synthase homolog ywnE - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: D5-D6c-1997 #sequence_revision 05-D6c-1997 #text_change 09-Jul-2004
C;Accession: G70063
R;Kunst, F.; Gasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter.
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galler
i, Harwood, C.R.; Henaut, A.; Hibbert, M.; Holsappel, S.; Hosnow, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kunano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucell
Y; M.; Ogawar, A.; Odwega, B.; Park, S.H.; Parro, V.; Pohl, T. T.M.; Portetelle
R; Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
a; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Withlors: Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451
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                                                                                                                                                                                                                                                                                                                                                                        107 WRNDISGRLLFNLMYLAAERGVRVRLLLDDDNNTRGLDDLLLAL-DSHPNIEVRLFNPFVL
                                                                                                                                                                                                                                                                                                                                                                                                               LDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGK-----GLQALGYNDETSRHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLR-YRETVE-QSPLYQK-----IQTGRIDWQSVQTRLISDTPAKGLDRDRRKP-PIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRLODALKOPEKSVYLVSPYFVPTKSGTDALAKL--VQDGIDVTVLTNSLQATDVAAVHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- TSLHAKTFIVDGK
                                                                                                                                                                                                                                   SRHFNTSKPVLLDNILQIRHTPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYI
                                                                                                                                                                                                                                                                          RKWRALGY-----LIDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFAD
                                                                                                                                                                    Gaps
                                                                                              16.1%; Score 439; DB 2; Length 652;
28.0%; Pred. No. 1.5e-23;
tive 69; Mismatches 200; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NEPEAKLWKRIAAKILSLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --APRKKLPGLYKLNYSVGKLSE--ALPVLDLWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 GYVKY-RKPLLKAGIKLYELQP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---NHAVPATKDKGLTGSSV--
A,Gene: XF1087
C,Superfamily: cardiolipin synthase
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19;

Gaps

162;

Length 494;

28

-----YNNAAFLTT 129

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Cardiolipin synthase homolog lin0008 [imported] - Listeria innocua (strain Clip11262) (Species: Listeria innocua (Species: Listeria innocua (Species: Listeria innocua (Species: Listeria innocua (Species: Listeria innocua (Species: Listeria dinocua (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria) (Species: Listeria
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A; Residues: 1-504 <GLA>
A; Residues: 1-504 <GLA>
A; Residues: 1-504 <GLA>
A; Cross-references: UNIPROT: 092FU5; UNIPARC: UPI00000CC0B3; GB: AL592022; PIDN: CAC95241.1
A; Experimental source: strain Clip11262
C; Genetics:
A; Gene: lin0008
C; Superfamily: cardiolipin synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | | : | : | : | 326
278 VNALQLRFILDMNS----QATRDHISYDDRYFPDVNSGGTIGVQIASSGPDEE----- 326
                                                                                                                                                                                                                                                                                                                                                                        119 LMYLAAERGVRVRLLLDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----RINRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFA---DLDILATGSV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGEVSHDFDRYWASHSAHNATR------IIRSGNIGKGLQALGYNDETSRHALL 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 RYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEK 335
                                                                                                                                                                                                                                                          DNILQIRHTPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFN
                                                                                                                                                                                                                                                                                              4 DPKIQAMPSETISP-----MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 SKLPLINLRMNRNHRKIVVIDGQIGYVGGFNVGDEY--LGKSKKFGYWRDTHLRIVGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVV
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11.0%; Score 300; DB 2; Length 504;
Best Local Similarity 23.0%; Pred. No. 1e-13;
Matches 118; Conservative 76; Mismatches 210; Indels 108;
                                Query Match
11.3%; Score 308; DB 2; Length 49.
Best Local Similarity 23.2%; Pred. No. 2.6e-14;
Matches 119; Conservative 76; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456 IESPKIAEQMERTLAD-----TTPEYAYR 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :||::::: | | INDQOIAKKLKQAFIDDLAVSSELTKARYAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: AI1433
A;Status: preliminary
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              A;Residues: 1-494 <KUR>
A;Residues: 1-494 <KUR>
A;Cross-references: UNIPROT:099SG9; UNIPARC:UPI0000D778F; GB:BA000018; PID:gl3701883;
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1891
C;Superfamily: cardiolipin synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SA1891 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #text_change 09-Jul-2004
C;Accession: F9001
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; oma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, I.c.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Reference number: A89788; MUID:21311952; PMID:11418146
A;Recession: F90001
A;Status: preliminary
A;Mocessioule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 HSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDSHPNIEV 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 LODALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVK 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 NDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGR 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSE------329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------KEDLL----VSRKFTYEEYLQ 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERTESRHFNTSKPVLLDNILQIRHTPHNNGL----SDIYLLDDPHEALAARAALIESAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 TVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRS------GNIGKGLQALGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386 YRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRS
A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Accession: G70063
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 25.3*
Matches 126, Conservative
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16;

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Qy         199 GGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRI 250           Db         250 GGLNIGEEYRSNTPDFRVWRDTHIKITGQAVIELQESFLNDWYMENQAGAADGF 304           Qy         251 IRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPA 310           Db         305 ISESGSKQYFSPUMGDEWAQVIYGGPVDKEKWVRDS 341           Qy         311 KGLDRDRRKPPIAGRLQPEKSVIVSPYFVTKSGTDALAKLVQDGIDVTVLTNS 370           Qy         342MLDLIDSAKESVWIVSPYFVPDEESLAVIRRVAMSGVDVRVIIPG 386	371 LQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVD 	QY 431 GKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQW 490  D 429 GTRAAIGTANFDVRSFRLNHELMVFLYDESEAMHHLKRDFKKDFEDSRL 477  QY 491 HDPATKKTYPNEPEAKLWKRIAAKILS 517	478FTWKDMENKPLLTRIKEVLSSLLS	AII762 cardiolipin synthase homolog lin2646 [imported] - Listeria innocua (strain Clip11262) C.Species: Listeria innocua C.Sate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C.Accesion: AI1762 R.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker	.; Dominguez-Bernal, G.; Duchaud, E.; Durand, b.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Malok, C.; Schlueter, T.; Simos, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Recession: Al1762 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-482 cGLA> A;Residues: 1-482 cGLA> A;Residues: Lastreferences: UNIPPOT:Q927Z0; UNIPARC:UPI00000CC933; GB:AL592022; PIDN:CAC97873.1; A;Experimental source: strain Clip11262 C;Genetics: A;Genetics: A;Superfamily: cardiolipin synthase	Query Match 10.7%; Score 292; DB 2; Length 482; Best Local Similarity 25.8%; Pred. No. 3.5e-13; Matches 109; Conservative 56; Mismatches 164; Indels 94; Gaps 15;	Oy 74 SDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLL 133 :::	OY 134 LDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADN 193 DD 179 YDAMGSRTTKKSFFRTFEKNGGLVRPFFPSKLPLINF-RLNYRNHRKLAIIDG 230	OY 194 RATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRS 253	OY 254 GNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTG-RIDWQSVQTRL 304	QY 305 ISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDV 364
Qy 74 SDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLL 133	246 NATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLI 305                 : : : : : : : : : : : :	QY 306 SDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVT 365	382 VIIPGKGDRGISFHGSNAYVKTMIEAGAKMYAYADDSFVHAK 423 426 TEIVDGKRIFIGSFNLDDRSARINTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKH 485	Db 424 AMLVDÖTRAAIGTANFÜVRSFRINHELMVFLYDESEAMLHLKRÜFKKÜFED 474  Qy 486 NRLQWHDPATRKTYPNEPEAKLWKRIAAKILS 517  CD	RESULT 16 A11075 Cardiolipin synthase homolog lmo0008 [imported] - Listeria monocytogenes (strain EGD-e) Cardiolipin synthase homolog lmo0008 [imported] - Listeria monocytogenes C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: A11075 C;Accession: A11075 C;Accession: A11075 C;Accession: A11075 C;Accession: A11075 C;Accession: A11075 C;Accession: A11075 C;Accession: A1075 C;A	PROT: Q8YAV5; UNIPARC: UPI0000055661; GB:NC_003210; PIDN: CAC98223.1		Query Match 10.8%; Score 294.5; DB 2; Length 504; Best Local Similarity 23.5%; Pred. No. 2.5e-13; Matches 119; Conservative 72; Mismatches 207; Indels 109; Gaps 17;	OY 19 KTRSLISLCLILCSCSSWLPPLEERTESRHFNTSKPVLLDNILQIRHTPHNNCLSDIYL 78	OY 79 LDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNN 138	OY 139 TRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATIL 198

8 6 8 6 8 6	365 TVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHA 424	RESULT 19 G89906 hypothetical protein SA1155 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: G89906 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogn ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K., Lancet 357, 1225-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
RESULT AG1387 cardio C; Spec C; Date C; Acce R; Glass R; Glass B; Dom D; Dom Science Science	RESULT 18 AG1387 cardioliptin synthase homolog lmo2503 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Decies: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AG1387 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker J Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H. Science 294, 849-852, 2001	
A, Author, C. O. A, Titl	iors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, e: Comparative genomics of Listeria species.  rence number: AB1077; MUID:21537279; PMID:11679669	Query Match 10.5%; Score 284.5; DB 2; Length 505; Best Local Similarity 21.7%; Pred, No. 1.3e-12; Matches 103; Conservative 79; Mismatches 158; Indels 135; Gaps
A; Acce A; Stat A; Mole A; Resi	ission: Aulak us: preliminary cule type: DNA dues: 1-482 <gla></gla>	Qy 63 QIRHTPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYL 122 
A; Cros A; Expe C; Gene A; Gene	s-references: UNIPROT:08Y4E3; UNIPARC:UPI0000055715; GB:NC_003210; PIDN:CAD00581.1 rimental source: strain EGD-e tics: . inc.503	QY 123 AAERGVRURLLLDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTD 176
C; Supe	•	
, yo	SDIXLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLL 13 :::	233 HOFDKYMASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSP
3 & 6	NEVELS VOCASER DALLANDIERANDAINITITERSDELGNKLMRVLEKKAAAEGLNVKII 17 LDDNNTRGLDDLLLALDSHPNIEVRENFVLRKWRALGYLTDFPRLNRRWHNKSFTADN 19	286 LYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSP
a & i	*DAWGSKTIKASFFKIFORNGGLVKFFFSKLPLINF-RLNYRNHRKLAIIDG 23 RATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRS 25	
ga Vo	231 DVGYIGGFNIGDEYLGASKKFGYMPATHLRVH 262 254 GNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTG-RIDWQSVQTRL 304	Qy 403 NHAVPATKDKGLIGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIA 462
oy Oy	263 GKAVYAMÓTRFIMDWNSASSTHKIDYKARÝFPTFHGKGHTSMÓIVSGAPDSEWÖQIKNGY 322 305 ISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDV 364   III	Qy 463 EQMERTLADTTPEYAYRVTLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILS 517 
9	323 IK	RESULT 20 H86744 cardolipin synthase [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C:Species: Lactococcus lactis subsp. lactis
දු දු	KIAEQMERTLADTTPE-Y ::::::  QWVQKLEDAFLEDILKSYQLTPELY	C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004 C;Accession: H86744 C;Accession: A: Wincker, P:; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl G;Roome Res. 11, 731-753, 2001
oy O	477 AYR 479 	A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: H86744 A;Status: preliminary

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A;Cross-references: UNIPROT:09K6C6; UNIPARC:UPI0000C42DC; GB:AP001520; GB:BA000004; NIDI
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiolipin synthetase BH3803 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C84125
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 TDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATK 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERGVRVRLLLD----DNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 VSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKI 290
                                                                                                                                                                                     NRRMHNKSFTADNRATILGGRNIGDEYFKVGEDT----VFADLDILATGSVVGEVSHDFDR
   118 NIMYLAAERGVRVRLLLDDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDF
                                                    -----ETILKPSYLSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                          291 QTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 DKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLA
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                                                                                                                                               P----RINRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFA---DLDILATGSVVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHTPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAA
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A, Gene: BH3803
C, Superfamily: cardiolipin synthase
                                                                                                                                                                                                                                                                                                                                                                   290 LQLIFLRDWAHETG-----
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A; Residues: 1-398 <STO>
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C.Species: Bacillus halodurans
C.Species: Bacillus halodurans
C.Species: Bacillus halodurans
C.Accession: B84007
B.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic. Acids Res. 28, 4317-431, 2000
A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Accession: B84007
A;Accession: B84007
A;Accession: B84007
A;Residue: preliminary
A;Molecule type: DNA
A;Residues: 1-503 < STO>
A;Cross-references: UNIPROT:09K8Z4; UNIPARC:UPI0000127B9A; GB:AP001516; GB:BA000004; NIE
A;Experimental source: strain C-125
C;Genetics:
A;Genetics:
Molecule type: DNA
A;Residues: 1-481 <STO>
A;Residues: 1-481 <STO>
A;Cross-references: UNIPROT:Q9CGY2; UNIPARC:UPI00000C695C; GB:AE005176; PID:g12723898; A;Cross-references: strain IL1403
C;Genetics:
A;Gene: clsA
C;Superfamily: cardiolipin synthase
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                                                                                                                                                                                                                                                                                           Query Match
10.4%; Score 282.5; DB 2; Length 4
Best Local Similarity 22.5%; Pred. No. 1.7e-12;
Matches 104; Conservative 76; Mismatches 167; Indels
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: #B8271
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: #B82711
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-467 <cIns.
A;Residues: 1-467 <cIns.
A;Cross-references: UNIPROT:09PE19; UNIPARC:UPI00000C265D; GB:AE003954; GB:AE003849; NI
A;Experimental source: strain 95C
A;Cross-references: UNIPROT:09PE19; UNIPARC:UPI00000C265D; GB:AE003954; GB:AE003849; NI
A;Experimental source: strain 95C
A;Experimental source: strain 95C
A;Experimental source: strain 95C
A;Experimental source: strain A.R.P.; Racincani, A.D.; Ferreita, A.J.S.
Submitterd to GenBank, Univ. 2000
A;Authors: Marchia, A.M.B.; Madeira, H.M.F.; Marchia, A.J.S.
Submitterd to GenBank, Univ. 2000
A;Authors: Marchia, B.M.F.; Matsukuma, A.Y.; Krieger, J.E.; Kuramae, E.E.; Miyaki, C.Y.
A;Authors: Marthib; E.M.F.; Matsukuma, A.Y.; Mench, G. Gliveira, R.C.; Palmieri, A;Authors: Marthib; B.M.F.; Matsukuma, A.Y.; Mench, G. Santelli, R.V.; Sawasa A;Authors: Anako, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa A;Authors: Annuber: Assiva, A.C.R.; da Silva, A.M.; Silva, A.M.; Silva, A.D.; A.C.R.; da Silva, A.M.; Silva, A.M.; Silva, A.D.; A.C.R.; Andrerence number: Assiva, A.M.; A.D.; A.C.R.; da Silva, A.M.; Silva, A.M.; Silva, A.M.; Silva, A.D.; A.C.R.; Andrerence number: Assiva, A.M.; A.D.; A.C.R.; da Silva, A.M.; Silva, A.M.; Silva, A.M.; Silva, A.M.; Silva, A.M.; Silva, A.M.; Silva, A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.M.; A.M.; Silva, A.M.; Silva, A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M.; A.C.R.; A.M
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C;Superfamily: cardiolipin synthase
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submitted to the EMBL Data Library, August 1998
A;Description: Clostridium perfringens hem operon.
A;Reference number: Z22707
A;Accession: T43863
A;Accession: T43863
A;Accession: T43863
A;Accession: T43863
A;Reasidus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-476 <KOY>
A;Residues: 1-476 <KOY>
A;Cross-references: UNIPROT:Q9ZNC6; UNIPARC:UPI000016E0DF; EMBL:AB017186; PIDN:BAA74786.
A;Experimental source: strain NCTC8237; vegetative cell
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             413
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C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
     LAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKG
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                                         10.0%; Score 273; DB 2; Length 476; 24.3%; Pred. No. 8e-12; ive 79; Mismatches 167; Indels
                                                                                                                                                                                                                                                 363 -DYDFSIS----ERLOMEDLANRSFFHRIKE
                                                                                                                                                                                                                PEYAYRVTLDKHNRLOWHDPATRKTYPNEPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 PRSARLNTEMGVVIESPKIAEQME 466
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A;Gene: cls
C;Superfamily: cardiolipin synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.0%
Best Local Similarity 24.3%
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: T43863
                                                                                                                                                               314
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GAKRGLRAYQQCLRAH-GVEVHAMLPGGLR-WRRSG-----RMDLRNHRKIAVIDNRVA 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 YENAR-----DAVNTMIHLARRRVVLTTPYFVPDEATLSALRIAGTSGVDVQLILSESN 353
                                                                                                                                                                                                                                                                                                                                                                                    197 ILGGRNIGDEYFKVGEDTVFADLDILATGSVVG-EVSHDFDRYWASHSAHNATRIIRSGN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 LDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDV-TVLTNSL 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LHAKHLSVDD 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 DIALFGSINLDIRSFALNABIGMICYDSRIVGRLREVESD-----YLANACOLNLVEWO 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWH 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiolipin synthase PA5394 [imported] - Pseudomonas aeruginosa (strain PAO1) C; Species: Pseudomonas aeruginosa
                                                                                                                             78 LLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDD-
                                                                                                                                                                                                                                                          137 NNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRAT
                                                                 93;
   Length 467;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.9%; Score 270.5; DB 2; Best Local Similarity 27.3%; Pred. No. 1.2e-11; Matches 117; Conservative 56; Mismatches 162;
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cardiolipin synthase XF1209 [imported] - Xylella fastidiosa (strain 9a5c)

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sequencing of the Bacillus subtilis chromosomal region from 3
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C;Superfamily: cardiolipin synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // Match
Local Similarity 22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain 168
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A, Description: Cloning and se
A, Reference number: $55414
A, Accession: $55414
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 432-500 <GLA>
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560089
cardiolipin synthetase homolog ywiE - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: 860089; 855414; F70059
R;Cruz Ramos, H.; Boursier, L.; Moszer, I.; Kunst, F.; Danchin, A.; Glaser, P.
EMBO J. 14, 5984-5994, 1995
A;Title: Anaerobic transcription activation in Bacillus subtilis: identification of dist
A;Reference number: $60080; MUID:96112813; PMID:8846791
A;Accession: $60089
A;Accession: $60089
A;Accession: $60080
A;Accession: $60080
A;Residues: 1-500 <CRU>
A;Residues: 1-500 <CRU>
A;Residues: 1-500 <CRU>
A;Cross-references: UNIRROT:P45860; UNIPARC:UPI000060BCF; EMBL:Z49884; NID:8971335; PIC
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
R;Glaser, P.; Danchin, A.
submitted to the EMBL Data Library, May 1995
               Cybace: 13-Sep-200 #sequence_revision 13-Sep-2000 #text_change 03-001-2004
Cybacession: B8291
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor,
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Reference number: DNA
A;Residues: DNA
A;Residues: DNA
A;Residues: UNIPROT:Q9HTHO; UNIPARC:UP100000C5FDF; GB:AE004952; GB:AE004091; NIL
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Cyberfamily: cardiolipin synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKP 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 IEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGEDT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 INAAHERVWITSPYFVPDEAVMAALRLAVLRGVDVRLLIPS--RPDHRTVYAASSLYALE 391
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 WLPPLEERTESRHFNTSKPVLLDNILQIRHTP--HNNGLSDIYLLDDPHEALAARAALIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 490;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 PLAPWRDTHMELRGPAVACLQESFAEDWYWATHSL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 9.9%; Score 26%; DB 2; al Similarity 24.5%; Pred. No. 1.9e-11; 111; Conservative 60; Mismatches 186
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A;Cross-references: UNIPARC:UP1000016E83F; EMED:Z49782; NID:g485752; PIDN:CAA89861.1; PID R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, E.; Broon, S.; Brooullet, S.; Buschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A;Authors: Foulgar, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galleri, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Levine, A.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell, Y.; M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadaie, V.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serox akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Yasumoto, K.; Yata, K.; Yoshida, K.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Wilters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Yasumoto, K.; Yata, K.; Yoshida, K.; A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:980440133; PMID:934377 A; Cross-references: UNIPARC: UP1000060BCF; GB: 299123; GB: AL009126; NID: 92636240; PIDN: CA 86 LAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDL 145 EYFKVGEDTVFADLDILATGSVVGEVSHD-FDRYWASHSAHNATRIIRSGNIGKGLQALG 264 -----ISRDPYIGFWRD-----THLRLEGEIVQTLHAIF 293 318 RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA 377 332 MKESMSDLYYEMISSAQKSIWIATPYFVPNESIRTALKAAATKGVEVRVWVP--EKNDSF 389 AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG 437 390 LTQYASRSYFPELLLEGIEVYSYQ------KGF------MHQKVMIIDGDLASVG 432 82 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA FPDIFKAMRKAESYIHIEYYMFKSDMLGRGMDIMMEKARQGVEVRFLYDAAGSMKLARR 146 LLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGD 265 YND--ETSRHALLRYRE----TVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDR ---IYLLDDPHEA 94 RMYNREK---LRKLFDKEETPEVTGLKDNQERFFTYSIRAAHMNINTKSNIKVLKNGEET Gaps Indels 131; ; Score 266.5; DB 2; ; Pred. No. 2.5e-11; 64; Mismatches 176; 294 MLDWEYVSNEVLDQEEYNTPVPVEGGGIYQIVATG---

cardiolipin synthetase (EC 2.7.8.-) [imported] - Brucella melitensis (strain 16M)

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65
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Matches
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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3539
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Arcersalen, Sequence of the facultative intracellular pathogen Brucella melitens A,Reference number: AD3252; PMID:11756688
A,Accession: AB3533
A,Accession: AB3533
A,Accession: AB3533
A,Residues: 1-492 <KUR>
A,Residues: 1-492 <KUR>
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A,Residues: 1-402 <KUR>
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A,Residues: 1-403 <KUR>
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K.; Lim,
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A;Accession: D83103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 RNDISGRILFNIMYLAAERGVRVRILLDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 WRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFK-VGEDTVFADLDILATGS 226
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23.0%; Pred. No. 4.1e-11;
tive 69; Mismatches 180;
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                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: II
C,Superfamily: cardiolipin synthase
C,Keywords: transferase
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Matches 98; Conservative
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A;Molecule type: DNA
A;Residues: 1-359 <STO>
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A,Cross-references: UNIPROT:Q9HW62; UNIPARC:UPI0000CSCCA; GB:AE004850; GB:AE004091; NI A,Experimental source: strain PAO1
A,Experimental source: strain PAO1
A,Genetic PA4339
C,Superfamily: cardiolipin synthase
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R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4833-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium ClA;Reference number: A96900; MUD:21359325; PMID:21359325
A;Accession: E97307
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-510 cKUR>
A;Residues: 1-510 cKUR>
A;Experimental source: Clostridium acetobutylicum ATCC824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRK 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 HSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSF 439
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                                                                                                                                                                                                                                                                                                                                                        ------IMLATPYFLPTWKVRRALRKAAQRGVEVRLLLAG-RLTDHAPV
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                                                                                                                                                                                                                                                        92;
                                                                                                                                                                                       Length 359;
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C,Superfamily: cardiolipin synthase
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Qy 327 QDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKY 386	C. Accession: G22171 C. Accession: G2217 C. Accession: G2217
Db 219 YHKELEKIGIKCCVFNPLIPWSF-KFNNRDHRKIAVIDGLVGFTGGINLSD 269  206 EYF-KVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGUIGKGLQALG 264	SULT 30  SULT 30  SULT 30  SULT 30  SUCT 30  SPECIES: Nostco ED. PCC 7120  Note: Nostco ED. PCC 7120  Note: Nostco ED. PCC 7120  Note: Nostco ED. Strain PCC 71  ARACOSION: AH233  A RES: 8, 205-213, 2001  Title: Complete Genomic Sequent  Reference number: AB1807; MUID  ACCESSION: AH233  A RES: 8, 205-213, 2001  A RES: 8, 205-213, 2001  A RES: 8, 205-213, 2001  A RES: 8, 205-213, 2001  A RES: 8, 205-213, 2001  A RES: 9, 205  A RES: 9, 205  A RES: 9, 205  A RES: 9, 205  A RES: 9, 205  A RES: 9,

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A,Reference number: S55414
A,Accession: S55419
A,Status; preliminary
A,Molecule type: DNA
A,Beatus: preliminary
A,Molecule type: DNA
A,References: UNIPARC:UPI0000060BCA; EMBL:Z49782; NID:g853752; P1
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R; Heiger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Saddie, Y.; Sato, T.; Scholoni, A,; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Tanakoshi, A.; Alaunopele genome sequence of the Gram-positive bacterium Bacillus subtilis
A,Accession: C70060
A,Residues: L-398 -KUN>
A,Residues: L-398 -KUN>
A,Residues: L-398 -KUN>
A,Residues: L-398 -KUN>
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A,Residues: R-398 -KUN>
A,Residues: L-398 -KUN>
A,Residues: R-398 -KUN>
A,Residues: L-398 -KUN>
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A,Residues: R-398 -KUN
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probable phospholipase ybhO [imported] - Salmonella enterica subsp. enterica serovar Ty
C;Species: Salmonella enterica subsp. enterica serovar Typhi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 SDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDDNNTRGLDDLLLALDSHPNI EVRLFN----PFVLRKWRALGYLTDFPRLNRRMHNKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 IIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRI------DWQSVQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.6%; Score 235; DB 2; Length 398;
Similarity 20.7%; Pred. No. 3.3e-09;
33; Conservative 71; Mismatches 178; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : | : ::|:
-KKSELLTMEDFSKRTFRQRPAEWLGRALS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKHNRLQWHDPATRKTYPNEPEAKLWKRIA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: ywjE
C,Superfamily: cardiolipin synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S:
Matches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
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                                                                                                           C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AG0266
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
Geno-Tarraga, A.W.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Reference number: AB0001; WUID:21470413; PMID:11586360
A;Accession: AG0266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q8ZE12; UNIPARC:UPI0000CD8B3; GB:AL590842; PIDN:CAC90995.1;
C;Genetics:
C;Genetics:
C;Superfamily: cardiolipin synthase
C;Superfamily: cardiolipin synthase
C;Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  m
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C;Species: Bacillus subtilis
C;Date: 15-Uul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S55419; C70060
R;Glaser, P.; Danchin, A.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning and sequencing of the Bacillus subtilis chromosomal region from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | | | : | : | | | : | | | STARWLSELK---ECQHIFANSNSEVASPLFQLCERRQGINGVKGNQLQLLTTTDDTLKA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 VLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELOPNHAVPATKDKGLTGSSVTSLHAK 425
                                                                                   - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAMMRNAGIEVV------EALKVNVFRMFL-------RAMDLRQHRKIVLIDN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 RATILGGRNIGDEYFKVGEDTVFADLDILA-----TGSVVGEVSHDFDRYWASHSAHNAT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 RII----RSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIVP--RENDSMMVRWASRAFFTELLNAGVKIYQF------EGGL-----LHSK 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTL--- 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYLVDGQLSLVGTVNLDMRSLWLNFEITLVIDD----DGFGADLAQVQDDYIARSALLDG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCSSWLPPLEERTESRH-FNTSKPVLLDNILQIRHTPHN-NGL--SDIYLLDDPHEALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAALIESAEHSLDLQYYIWR-NDISGRLLFNLMYLAAERGVRVRLLLLDDNNTR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.9%; Score 241.5; DB 2; Length 486; 22.5%; Pred. No. 1.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 180;
                                                                                   cardiolipin synthetase (EC 2.7.8.-) [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERWNKRPLWHRVTERLFY 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-486 <KUR>
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Best Local S:
Matches 112
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Indels 121; Gaps

282

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Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-492 <KUR>
A;Cross-references: UNIPROT:Q8UCJ8; UNIPARC:UP10000D1F08; GB:AE008688; PIDN:AAL43473.1;
A;Experimental source: strain CS8 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiolipin synthase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004 C;Accession: AC2882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 GYNDETSRHALLRYRETVEQSPLYQKI--QTGRIDWQSVQTRLISDTPAKGLDRDRRKPP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 WRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDDNNTRGLDDLLLALDSHPNIEVR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 LFNPFVLRKWRALGYLTDF-----PRLNRRMHNKSFTADNRATILGGRNIGDEY-- 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----FKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQAL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 IAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHS 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------EAGGKVTAFITSRNTLTKTRLNYHLHRKIVVIDGQIGWTGGFNVGDQYIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 NSKKFGFWRDT------HGRIVGTAAFGLQE------TFIRDWNV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 RRFBAMK-TLGDRV--TRHALTTGNGIEPLVSGD---VAYAAMLBAIGBAKRSIILETYI
                                                                                                                                                                                                                                                                                                                                                                                         48 RHFNTSKPVLLDNILQIRHT-PHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYI
                                                                                                                                                     43 ERTESRHFNTSK--PVLLDNILQIRHTPHNNGLSDIY--LLDDPHEALAARAALIESAEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match

8.3%; Score 224.5; DB 2; Length 4.

Best Local Similarity 23.0%; Pred. No. 2.6e-08;

Matches 96; Conservative 56; Mismatches 190; Indels
                                                                                                                                                                                                                                        104 ERLLKRYFNNMERTPLCRGNKVNF----YLNG-EDKFSALFDD---
                       Pred. No. 1.8e-08;
; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381 ATQYYANYLHKHGVKIYNYTNGF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 DIRSYELNFEISAFCYDETVAKEMSRT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPRSARLNTEMGVVIESPKIAEQMERT
                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: cls
A,Map position: circular chromosome
C,Superfamily: cardiolipin synthase
                       22.4%;
                                                                     Conservative
                       Best Local Similarity
Matches 100; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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F86771
cardolipin synthase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86771
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 71-753, 2001
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Reterence number: A86625; MUID:21235186; PMID:11337471
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-487 cs70>
A;Cross-references: UNIPROT:Q9CGC3; UNIPARC:UPI00000C69C8; GB:AE005176; PID:g12724139; E
A;Genetics:
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A; Note: this species has also been called Salmonella typhi
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-May-2004
C; Accession: 410598
R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Atterence number: AB0502; MUID:21534947; PMID:11677608
A; Accession: A10598
A; Accession: A10598
A; Residues: 1-413 < PAR>
A; Residues: 1-413 < PAR>
A; Residues: 1-413 < PAR>
A; Cross-references: UNIPARC:UPI000005A0E6; GB:AL513382; PIDN:CAD05259.1; PID:gl6502026; C; Genetics: ybho
C; Superfamily: cardiolipin synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 LDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFD------RYWASH 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIAFVGGINYSAEHMSDYGPQAKQDYAVRVEGPVVADIL-QFEVENLPGQSPARRWWKRH 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------EENRHPGEAQALFVWR-------- 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | :: | | :: | | | :: | | | | :: | | :: | | | :: | | :: | | | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.4%; Score 228; DB 2; Length 413; Best Local Similarity 22.2%; Pred. No. 1.1e-08; Matches 92; Conservative 55; Mismatches 163; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 ARRĠVSVKLIVQG--EPDMPIVKVĠARLLYNYLVKGĠVQVYĖYRRR----
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106

Gaps

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SP 03	167 KWRALGYLTDFPRLNRRWHNKSFTADNRATILGGRNIGDEY-FKVGEDTVFADLDILATG 225 	RESULT 38
o, du	226 SVVGEVSHDFDRYMASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEGSP 285 273 PVVSDFFSIAAEDWRFTTGE	B83377 probable phospholipase PA2155 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence revision 15-Sep-2000 #text change 09-Jul-2004
රු දු		C; Accession: B83377 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lir Lory, S.; Olson, M.V.
& 8	и п	Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: B83377
& g	406 VPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIA 462 	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-401 <sto> A;Cross-references: UNIPROT:Q911W0; UNIPARC:UP100000C55D9; GB:AE004642; GB:AE004091; NI</sto>
RESULT 37 B97658 cardiolipin	CSB. Cereon	A;Genetics: A;Genetics: A;Gene: PA2155 C;Superfamily: cardiolipin synthase
C;Specie C;Date: C;Access	<pre>Agrobacterium tumefaciens Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 B97658</pre>	Query Match 8.2%; Score 224; DB 2; Length 401; Best Local Similarity 22.8%; Pred. No. 2.1e-08; Matches 98; Conservative 59; Mismatches 184; Indels 88; Gaps 11;
A, Goodne A, ; Liu Science A:Title:	r, b.; hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; 294, 2323-2328, 2001 Genome Segmence of the Plant Parhogen and Richechnology agent Agrobatication to	INNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERG 1
A;Refere A;Access A;Status	A;Reference number: A97359; MUID:21608551; PMID:11743194 A;Accession: B97658 A;Status: preliminary A:Molecule true. Dan	128 VRVRLLLDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRHNK
A, Residu A, Cross-	cs: 1-492 <kur> references: UNIPROT:Q8UCJ8; UNIPARC:UPI00000D1F08; GB:AE007869; PIDN:AAK88219.1;</kur>	Db 63 VEVQVTVDGYGTASLSPDYLARLTASGVRVHLFDPRPRLLGMRTNLFRRLHRK 115 Qy 188 SFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRVWASHSAHNA 247
C;Geneti A;Gene: A;Map po	AGR: 4515 sition: circular chromosome	
C, Superf Query	<pre>amily: cardiolipin synthase Match 8.3%; Score 224.5; DB 2; Length 492;</pre>	Qy 248 TRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRL 304
Best Local S Matches 96	imilarity 23.0%; Pred. No. 2.6e-08; Conservative 56; Mismatches 190; Indels	305 ISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDV
ò 5	48 RHFNTSKPVLLDNILQIRHT-PHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYI 106	:    :   :  :
3 8		OY 365 TVLINSLQATIVAANHSTAT KRKKELKAGIKLYELQPNHAVPATKDKGLTGSSVTS 421  Db 244 DLVLQGMPDMPLVRLCSRLLYDYLLREGVRIHEYCQRP281
Dβ		Qy 422 LHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVT 481
දු දු	167 KWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGDEY-FKVGEDTVFADLDILATG 225 220 GLRLEYANLETHRKLLVDGRIAESGRNIREGFTLEFGRSOGHTHFRITG 272	Db 282 LHGKVAVIDDDWSTIGSSNLDPLSLSLNLEANLVIRDVAFNGQLYQHLRELARRHCRRIS 341
ò	SVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSP	342 REHARRGYW
qa		RESULT 39
රු සි	286 LYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFV 345 ::	E64815 ybhO protein - Escherichia coli (strain K-12) N;Alternate names: protein b0789
oy Oy	346 PTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHA 405	C.Species: Escherichia coli C.Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004 C.Accession: E64815 R.Blatther, F.R.: Plunkett III. G.: Bloch. C.A.: Perna. N.T.: Burland. V.: Rilev. M.: CA
δ q	406 VPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIA 462 	

--PLHG 291

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11 GYGSPDLSDEFUNELTAAGVVFRYYDP----RPRLFGMRTN----VFRRMHRKIVVIDARI 123
                                                                                                                                                                        HNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRL 304
                                                                                                                                                                                                                                                                     305 ISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDV 364
                                                                                                                                                                                                                                                                                                                                                                    365 TVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHA 424
                                                                             TILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFD-------RYWASHSA
                                                                                                                                                                                                                                                                                                   124 AFIGGLNYSAEHMSSYGPEAKQDYAVRLEGPIVEDIL-QFELENLPGQSAARRWWRRH--
                                                                                                                                                                                                                       425 KTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLAD 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 KVALMDDHWATVGSSNLDPLSLSLNLEANVIIHD----RHFNQTLRD 334
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D85587
probable synthetase ybhO [imported] - Escherichia coli (strain O157:H7, substrain EDL933
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85587
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Dimalanta, E.; Potamousis, K.; Apodaca,
Natite: 409, 529-533, 2001
A;Tite: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Recession: D85587
A;Retus: preliminary
A;Molecule type: DNA
A;Retaus: preliminary
A;Reterences: UNIPROC:P7571; UNIPARC:UP1000013A35B; GB:AE005174; NID:g1251377B; E
A;Experimental source: strain O157:H7, substrain EDL933
A;Gene: ybbo
C;Superfamily: cardiolipin synthase
A;Accession: E64815
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: nucleic acid sequence not shown; translation not shown
A;Status: Lyel: DNA
A;Rosiques: 1-413 < BLAT>
A;Cross-references: UNIPROT:P75771; UNIPARC:UPI000013A35B; GB:AE000181; GB:U00096; NID:g
A;Access-references: strain K-12, substrain MG1655
C;Genetics:
A;Gene: ybho
C;Superfamily: cardiolipin synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                             136 DINTTRGLDDLLLALDSHPNIEVRLFVDFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYGSPDLSDEFUNELTAAGVVFRYYDP----RPRLFGMRTN---VFRRMHRKIVVIDARI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 TILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFD------RYWASHSA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRL 304
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Best Local Similarity 21.9%; Pred. No. 3.5e-08;
Matches 89; Conservative 53; Mismatches 171; Indels 94; Gaps
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1 Similarity 21.9%; Pred. No. 3.5e-08;
89; Conservative 53; Mismatches 171; Indels
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Best Local Similarity
Matches 89; Conserva
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2003bs:\* geneseqp2004s:\*

geneseqp2005s:\*

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
				-		
-	2712	99.7	525	9	ABP79466	Abp79466 N. gonorr
7	2643	97.2	525	Ŋ	ABB78070	Ami
m	2606.5	95.8	507	٣	AAY75751	Aay75751 Neisseria
4	2586	95.1	508	ო	AAY75753	
Ŋ	2573	94.6	508	٣	AAY75752	Aay75752 Neisseria
9	831.5	30.6	543	œ	ADL04719	
7	790	29.0	564	7	AB075163	Pse
ω	632	23.2	502	~	AAW55452	Aaw55452 H. pylori
6	632	23.2	502	7	AAW55550	Ξ
10	590	21.7	428	~	AAW98378	Aaw98378 H. pylori
11	493.5	18.1	271	9	ADA34272	Ada34272 Acinetoba
15	478.5	17.6	275	9	ADA34304	Ada34304 Acinetoba
13	419	15.4	2519	7	ABM88218	Abm88218 Rice abio
14	409	15.0	321	9	ADA36398	Ada36398 Acinetoba
15	308	11.3	513	9	ABM71816	Abm71816 Staphyloc
16	296	10.9	486	7	ADG30702	
17		10.8	504	S	ABB49813	Abb49813 Listeria
18	291	10.7	495	ß	ABP39428	Abp39428 Staphyloc
19	291	10.7	495	ω	ADS04559	
20	287	10.6	482	ស	ABB49993	Abb49993 Listeria
21	286.5	10.5	493	'n	ABB32481	Abb32481 Staphyloc
22	286.5	10.5	493	7	ADC21336	Adc21336 Staphyloc
23	286.5	10.5	493	7	ADC25022	Adc25022 S. aureus
24	286.5	10.5	493	7	ADD52524	Add52524 Staphyloc

Abb32493 Staphyloc	Adc21402 Staphyloc		Add52590 Staphyloc	Abm71594 Staphyloc	Abb54276 Lactococc	_	Aaw55249 H. pylori		Abo75565 Pseudomon	Abo68379 Pseudomon			Ada36341 Acinetoba	Aab76548 Corynebac			Adf04432 Bacterial	Adh85779 Enterococ	Aaq81953 S. epider	Ε.
ABB32493	ADC21402	ADC25088	ADD52590	ABM71594	ABB54276	ABM97264	AAW55249	ABM69020	AB075565	AB068379	ABP39331	ADS05084	ADA36341	AAB76548	AAG92760	AAG80237	ADF04432	ADH85779	AAG81953	ADC94461
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RESULT 1

The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76716-ABP81046 represent nucleic acid molecules of the invention New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection. Antibacterial; infection; vaccine; gene therapy N. gonorrhoeae amino acid sequence SEQ ID 5462. ы :-Monaci Disclosure; Page 587; 815pp; English. Masignani V, ABP79466 standard; protein; 525 AA 12-FEB-2002; 2002WO-IB002069. 12-FEB-2001; 2001GB-00003424. (first entry) Neisseria gonorrhoeae. Fontana MR, Pizza M, WPI; 2003-058415/05. (CHIR-) CHIRON SPA. N-PSDB; ABZ40436. Sequence 525 AA; WO200279243-A2. 07-MAR-2003 10-OCT-2002. ABP79466; ABP79466 

Score 2712; DB 6; Length 525; Pred. No. 9.9e-240;

99.78;

Query Match Best Local Similarity

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Neisseria meningitidis, Neisseria gonorrheae, antigen; vaccine, antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                (Updated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVT
                                                                                                                                                                             The present sequence represents a p55 polypeptide. The specification describes p177, p88, p64, p55 and p46 polypeptides from Neisseria gonorrheae. The polypeptides are useful as vaccines, for preventing, protecting a female patient against, N. gonorrheae colonization or inflection. Such immunisation can prevent gonorrhea in women. (Updateć 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                     New polypeptide comprising p177, p88, p64, p55 or p46 from Neisseria gonorrheae, useful for preventing, or protecting a female patient against, N. gonorrheae colonization or infection.
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Pred. No. 2.2e-233;
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                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                  Claim 7; Page 120-121; 130pp; English
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               WPI; 2002-619227/66.
N-PSDB; ABQ78301.
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                                                                                                                                                                                                                                                                                                                        Sequence 525 AA;
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21-MAR-2000
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                                   MHTDPKIQAMPSETISPMKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDN
                                                                 MHTDPKIQAMPSETISPMKTRSLISLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDN
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Mismatches
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UNIV CALIFORNIA.
APICELLA M A.
EDWARDS J L.
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06-AUG-2001; 2001US-0310356P.
23-OCT-2001; 2001US-0344452P.
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BROWN E.
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 240 KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR
                                     RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA
                                                      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
                                                                                                                           360 AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
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Scalato E, Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis ORF 987 protein sequence SEQ ID NO:2978.
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Petersen J, Pizza M, Rappuoli R,
Tettelin H, Venter JC;
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09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                             , Mora M;
Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics.
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Pred. No. 4.6e-230;
1; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                             Masignani V,
Scalato E, S
                                                                                                                                                                                                                                                                                                                                                                             Hickey E,
Ratti G,
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                                                                                                                                                                                                                                                                                                                                                                          Fraser C, Galeotti C, Grandi G,
Petersen J, Pizza M, Rappuoli R,
Tettelin H, Venter JC;
                                                                                                                                                                                980S-0094869P.
980S-0098994P.
980S-0103749P.
980S-0103794P.
980S-0103794P.
                                                                                                                                    99WO-US009346
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antibacterial; gene therapy
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INST GENOMIC RES.
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                               Neisseria gonorrhoeae.
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                                                               WO9957280-A2
                                                                                                                                  30-APR-1999;
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Best Local S
Matches 505
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bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also used in gene therapy protocols
                                                                                                                   Gaps
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                                                                                                                   Indels
                                                                                             Length
                                                                                          Query Match
95.1%; Score 2586; DB 3;
Best Local Similarity 98.2%; Pred. No. 3.5e-228;
Matches 499; Conservative 4; Mismatches 5;
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                                                                    Sequence 508 AA;
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31-JUL-1998;
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynuclectides and polypeptides. AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynuclectides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynuclectides of the invention may also be
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                                                                                                                            Masignani V, Mora M;
Scalato E, Scarselli
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                                                                                                                                                                                                                  be useful antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 508;
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Pred. No. 5.5e-227;
5; Mismatches 6;
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                                                                                                                                                                                                                  Novel Neisserial polypeptides predicted to vaccines and diagnostics.
                                                                                                                            Hickey Ratti
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                                                                                                                            Grandi G,
Rappuoli R,
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97.8%; Prec
tive 5; N
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98US-0098994P.
98US-0099062P.
98US-0103749P.
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98US-0103796P.
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Matches 497; Conservative
                                                                                                    INST GENOMIC RES
                                                                                                                                         Petersen J, Pizza M,
Tettelin H, Venter JC;
                                                                                                                             Galeotti C,
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                         09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a barching to bind a P. aeruginosa mucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa sequences or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa sequences of Pseudomonas species using biochip technology. Sequences AB067826. The Reduction of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences AB067826. Sequence data for this patent did not form part of the printed sequence than sequence trom of the printed sequence. The sequence than a sequence them
                                                                                                                                                                            429 RQHSTTSLHAKAFAVDDDQIFIGSYNVDPRSANINTELGVLIKDSKLAGGLHKALSNSQA 488
                                                                                                                                                                                                                                                                    489 ITHQAYELKLDAKGNINWH-----TIENGOPVILHHEPHMNHKDRIIIWLAGLMPIDWL 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
QSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKL 357
                                                                                                 369 AKMGVEVRILTNSFDATDVGIVHAGYAHWRKQLLAAGVHLFEIKSSAQSIQDNENRFWRT
                            FWTEIDLIADNVIKLNGHSDPNEFLVSQLQTQLGQPSKKLSIISSYFVPTKEGIDTLITL
                                                                             358 VQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPN-HAVPATKDK--GL
                                                                                                                                                      TGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa polypeptide #7338.
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N-PSDB; ABD08734.
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27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRVRLLLIDD-NNTRGLDDLLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHN 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 IETLVKHDNKDDISGIKPVVFDELEKVKDSSDADRELRTYRQAMQNSTIGQDLLAQQVPF 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATRIIRSGNIG--KGLQALGYND-----ETSRHALLRYRETVEQSPLYQKIQTGRIDW 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid encoding an Moraxella catarrhalis polypeptide. The nucleic acid is useful for preparing a composition for diagnosing, preventing or treating infection caused by Moraxella catarrhalis. The present sequence represents the amino acid sequence of a M. catarrhalis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |::| |::| |::|| ||:||| ||:||| ||:||| ||:||| ||:||| PNQSG---YYPITTGANAFAARSTLTDVANQSIDIQYYIWHNDEAGQLMLKDLWEAADRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLISLLCLLLCSCSSWLP-----PLEERTESRHFNTSKPVLLDNIL----QIRHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid encoding a Moraxella catarrhalis polypeptide, paring a composition for diagnosing, preventing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.6%; Score 831.5; DB 8; Length 543; 35.9%; Pred. No. 6.3e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 35.9%; Pred. No. 6.3e-
94; Conservative 102; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 2405; 429pp; English.
                                    TYPNEPEAKLWKRIAAKILSLLPIEGLL
                                                                                                                                                    Ā
                                                                                                                                                                                                                                                                                                     Moraxella catarrhalis; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preparing a composition for diago
caused by Moraxella catarrhalis.
                                                                                                                                                ADL04719 standard; protein; 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-APR-2000; 2000US-00540236.
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                                                                                                                                                                                                                                                                M. catarrhalis protein #485
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                                                                                                                                                                                                                                                                                                                                             Moraxella catarrhalis.
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Matches 194;
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RN-KGLRYFEMLADYERIKKRMHNKLFIVDNFAVIIGGRNIGDNYFDNDLDTNFLDLDAL 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRYRETVEQSPLYQ-KIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPATRKTY----PNEPEAKLWK 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: ::| |::: :| |: :: :| |: :: :| 432 VLFDNPSFAKRVRLSLKDHA-QQSWHLVLYRH-RVIWE--ATEEGILIHEKNSPDTSFFL 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 IRHTPHNNGLSDIY------LLDDDPHEALAARAALIESAEHSLDLQYYIWRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKWRALGY---LIDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 KKVNDFIERFÇKYQYPIYYG-----NAIFLADLPAK-IDTPLYS-PIKIAFEKALKNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                              (ASTR ) ASTRA AB
                                                                                    N-PSDB; AAV24861
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 502 AA;
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28-OCT-1996;
         06-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                         R-TLADTTPEYAYRVTLDKHN---RLQWHD--PATRKTYPNEPEAKLWKRIAAKILSLLP 520
                                                                          68
                                                                                              94
                                                                                                                                                                                                                                                             272 RPIEDFLWRAPYPGEL------SARRKLQRYLRKESVKESGYIRHLFDRGDQPR
                                                                                                                                                                                                                                                                                                                                                                                           HNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSA
                                                                                                                                                                                                                    212 HNKLWLADGTAAIVGGRNLGDEYFNAKPEMNFTDLDLLGVGPIANQLSHSFDQYWNSAIS
                                                                                                                                                                                                                                                                                                                                                  -----LEERTESRHFNTSKPVLLDNILQIRHTP
                                                                                             50 ŘRFLLLALLALSGČASTPPPQPSSALPAEGTWLARQAB--------IQGŘDHP
                                                                                                                    69 HNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGV
                                                                                                                                       ---GOŚGFHLLGASEDAFVARAALIRAAORŚLDIOYYIVHDGLTTRALAYELLKAADRGV
                                                                                                                                                             RVRLLLDDNNTRGLDDLLLALDSHPNI EVRLFNPFVLRK----WRALGYLTDFPRLNRRM
                                                                                                                                                                                                                                                  245 HNAT----RIIRSGNIGKGLQALGYNDETSRHALLRY--RETVEQS----PLYQKIQTGR
                                                                                                                                                                                                                                                                                          I-DWQS----VQTRLISDTPAKGLDRDRRKPP--IAGRLQDALKQPEKSVYLVSPYFVPT
                                                                                                                                                                                                                                                                                                                                     KSGTDALAKLVQDG1DVTVLTNSLQATDVAAVHSGYVKYRKPLLKAG1KLYELQPNHAVP
                                                    Gaps
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                                                    70;
                               Length 564;
                                                   86; Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori ORF 02ae11612_33203250_c1_51 secreted protein.
                               DB 7;
                              29.0%; Score 790; 36.7%; Pred. No. 4
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                                                                         21 RSLISLLCLLLCSCSSWLPP----
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96US-00758731.
96US-00736905.
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                                                   200; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564
                                        Local Similarity
          Sequence 564 AA;
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02-APR-1996;
25-OCT-1996;
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26;

Length 502; Indels

23.2%; Score 632; DB 2; L 32.8%; Pred. No. 1.2e-48; ive 93; Mismatches 181;

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This sequence is a H. pylori secreted protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. C. a vaccine to prevent or treat H. pylori infection or to identify H. Dylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and distribution of H. pylori-specific artigens. The sequences of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify clikely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant complete mined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide to production, e.g. in E. coli hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14,94; Page 659-660; 1145pp; English
96US-00738859
96US-00761318
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64 IRHTPHNNGLSDIY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is a H. pylori secreted protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. 20 a vaccine to prevent or treat H. pylori infection or to identify H. 20 pylori polypeptide binding compounds, useful as potential H. pylori life cortivators or inhibitors. The DNA and probes derived from it may be used for the identification of H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays complements and distribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial CC from overlapping contigs generated by mechanically shearing the bacterial CC the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid complements protein sequences of interest, particular regions can be complemented from various OKF were analysed for significant con the predicted coding regions defined membrane proteins. Having identified and determined the sequences of interest, particular regions can be considered from H. pylori by PCK amplification for recombinant polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection.
                                                                                                                                                                                                                                                               Cytoplasmic, vaccine, prevention, treatment, infection, envelope, identification; binding compound, bacteria, life cycle, activator, inhibitor; duodenal ulcer disease, chronic gastritis, diagnosis.
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                                                                                                                                                                                                                              H. pylori ORF 01ce21104_33203250_c3_87 secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14,94; Page 755-756; 1145pp; English.
                                                                                                                              AAW55550 standard; protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from H. pylori by PCR am
n, e.g. in E. coli hosts
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96US-00736905
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96US-00761318
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            520
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Best Local Similarity 32.8
Matches 161; Conservative
                                          RLIKEWSKVLP 498
            RIAAKILSLLP
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                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith D, Alm RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASTR ) ASTRA AB.
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                                                                                                                                                                                               24-JUN-1998
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28-OCT-1996;
06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                        WO9737044-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-1997.
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                                                                                                                                                               AAW55550;
          210
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17;

Gaps

56;

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204
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                                                                                                                                                                                                                                                                                                         453
                                                                                                                                                                                                                                                                                                                                                                                 431
                                                                                                                                                                                                                                                                                                                                                                                                              VVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPATRKTY----PNEPEAKLWK 509
                                                                                                                                                                                                                                                                                                                                                                                                                              |: ::| |::: :| | : : : | | : : : | 432 VLFDNPSFAKRVRLSLKDHA-QQSWHLVLYRH-RVIWE--ATEGILIHEKNSPDTSFFL 487
                                                                                                                                                             223 ATGSVVGEVSHDFDRYWASHSAHNATRIIRS------GNIGKGLQALGYNDETSRHAL 274
                                                                                                                                                                                                                                                                                     334 EKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKA 393
           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Helicobacter polynucleotides - used to develop products for
the diagnosis, prevention and treatment of Helicobacter infections and
gastrointestinal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
                                                                                                                                                                                                                                                                                                                                                                   205 FFGGVASKAKESFENYWRFHRSIPVS-LLRTHKRLKNNVKEIAKLHEKIPISAEDANEFE
                                                                                                                                                                                                                                             264 KKVNDFIERFQKYQYPIYYG-----NAIFLADLPAK-IDTPLYS-PIKIAFEKALKNA
                                       110 DISGRILFNIMYLAAERGVRVRLILDDNNTRGLD----DLLLALDSHPNIEVRLFNPFVL
                                                                                                  166 RKWRALGY --- LTDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDIL
                                                                                                                                                                                                                                                                                                                                                 GIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oomen RP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kleanthous H, Al-Garawi A, Miller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US006371.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW98378 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIAAKILSLLP 520
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RLIKEWSKVLP 498
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(GENO-) GENOME THERAPEUTICS CORP.
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                                                                                                                                                                                                                                  Sequence 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1999;
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                                                                                                                Example;
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                    Breton
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                     inversion. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastris, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for diseases.
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                                                                                                                                                                                                                       116
                                                                                                                                                               151
                                                                                                                                                                                                                                                                                 307
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                                                                                                                                                                                                                                                                                                                                 217 SPKK-IDTPLYS-PIKIAFEKALKNAKDSVFIASSYFIPGKKMMKIFKNQISKGIELNIL 274
                                                                                                                                                                                                                                                                                                                                                            427
                                                                                                                                                                                                                                                                                                                                                                                                            ||||| :|| |: :|| |: :|| |: || || || || TNSLSSTDAIVVYGAWERYRNQIVRMGANVYEIRNDFFNRQIKGR---FSTKHSLHGKTI 331
                                                                                                                                                                                                                                                                                                                                                                                                  428 IVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNR 487
                                                                                                                                                                                  57
                                                                                                                                                               96 AEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLD----DLLLALDS
                                                                                                                                                                         HKNIEVKIFNPYYIRN-KGLRYFEMLADYERIKKRMHNKLFIVDNFAVIIGGRNIGDNYF
                                                                                                                                                                                                                                                                                                   ---HKRLK-NNAKEIAKLHEKIPISAEDKNOFEKKVNDFIDRFOKYOYPIYYGNAIFLAD
                                                                                                                                                                                                     HPNIEVRLFNPFVLRKWRALGY - - - LTDFPRLNRRMHNKSFTADNRATILGGRNIGDEYF
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                                                                                                                                                                                                                                                                                                                                                            TNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTF
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                            78;
                                                                                                                          Length 428;
                                                                                                                        21.7%; Score 590; DB 2; Length 42 32.3%; Pred. No. 6.7e-45; ive 80; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                 TSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRL------
                                                                                                                                                                                                                                                       OSWHLVVYR-----HRVIWEAVEEGIL 400
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          8; Page 581-583; 2054pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA34272 standard; protein; 271
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                                                                                                                                  Local Similarity 32.3
1es 145; Conservative
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                                                                                                       Seguence 428 AA;
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                                                                                                                                                                                                                                                                                                                          New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for baumannii present sequence represents the amino acid sequence of an A. baumannii protein.
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; Pred. No. 2.4e-36;
47; Mismatches 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0088701P.
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43.8%;
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                                                                                                                                2003-576092/54
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                                                                                                                                                                                                       N-PSDB; ADA30146
Bush
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for altering the an abiotic stress such as cold

English.

Katagiri F;

Goff SA,

Glazebrook J,

Cooper B, Gl N, Ricke D,

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abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
                                                                                                                                                                                                                                                                                                                                                                        Rice abiotic stress responsive polypeptide SEQ ID NO:6464.
                                                                                                                                                                                                                                                                                                                                 ABM88218 standard; protein; 2519 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-0300112P.
2001US-0314662P.
2001US-0325277P.
2001US-0332132P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2002; 2002WO-US019668
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                          Best Local Similarity
                                                                                                                   plants. The presen
baumannii protein.
                                                                                                                                                                                                                                                                                    EGLL 525
                                                                                                                                                                                                                                                                                                  EGFM 275
                                                                                                                                      Sequence 275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               WO2003008540-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-2001; 2
24-AUG-2001; 2
26-SEP-2001; 2
21-NOV-2001; 2
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                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                               Matches 100;
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                                                                                                                                                                                          35
                                                         Example;
                                                                                                                                                   Query Match
                                                                                                                                                                                                       354
                                                                                                                                                                                                                                                                                                                                              ABM88218;
                                            plants.
                                                                                                                                                                                                                                                                                                                     RESULT 13
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The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test blant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, osmotic stress cany of their combinations. The present sequence is used in the exemplification of the invention
                                                                                                                                                           responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
(SYGN ) SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 6464; 89pp;
                                          Briggs SP,
T, Provart
                                                                                                                WPI; 2003-248011/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2519 AA;
                                                                     Moughamer T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32
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                                                                                 New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 RIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       405 AVPATKDK-GLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAE 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                464 OMERTLADTTPEYAYRVTLDKHNRLOWHD--PATRKTYPNEPEAKLWKRIAAKILSLLPI 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THHTMDENLNKYAYKLKLDPNNHIYWQQETPKGPVIYKKEPEMKWWQKAGMKLLSWLPL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 478.5; DB 6;
Pred. No. 5.9e-35;
1; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
                                                                                                                                                                                            SEQ ID NO 5591; 328pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
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              WPI; 2003-576092/54.
N-PSDB; ADA30178.
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258
                                                                                                                                                                       471
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                                                                                                                                                                                                                                                                                                                                            259 GLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQS------VQTRLISDT 308
                                                                                                                                                                                                                                                                                                                                                                            TLLREGV--PTLPPASFRRPERVQR----VSAEANDMDFVSRSFVDTALPVASVRYVADL 642
                                                                                                                                                                                                                                                                                                                                                                                                              PAKGLDRDRRKPPIAG-----RLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQ--D 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IKL-----YELQP-----NHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFN 440
                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SGYVKYRKPLLKAG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  761
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                                                                                                                                                                                                                              :| || :| | ::|::|| | ::
ILGALSGAHQNFQLRVYNPTFGKARLNYFDYAGSVLCCFRRFNQRMHNKLLVIDDAIGVV
                                                                                                                                                                                                                                                                                                CSCSSWLPPLEER--TES-----RHFNTSKPVLLDNILQIRHTPHNNGLSDIYLLDDPHE
                                                                                                                                     ALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDD
                                                                                                                                                       LILALD-SHPNIEVRLFNP-FVLRKWRALGY----LTDFPRLNRRMHNKSFTADNRATIL
                                                                                                                                                                                                                                                                           GGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                   112;
15.4%; Score 419; DB 7; Length 2519; 28.2%; Pred. No. 5.5e-28; tive 76; Mismatches 186; Indels 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441 LDPRSARLNTEMGVVIESPKIAEQM-ERTLADTTPEYAYRV 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 GIDVTVLTNSLQATDVAAVH------
                                Conservative
                Local Similarity
nes 147; Conserv
                                                                                                                                                                                                                                                                                                           532
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ADA36398 RESULT

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ABM71816 standard; protein; 513
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                               ABM71816;
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                                                                                                                                                                                                                                                                                             New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARAALI ESAEHSLDLQYYIWRNDI SGRLLFNLMYLAABERGVRVRLLLDDNNTRGLDDLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGK-GLQALGYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLCSCSSWL--PPLEERTESRHFNTSKPVLLDNILQIRHTPHNNGLSDIYLLDDPHEALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------QGLTAFVALDDAFMSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLLQHTNFEIRLFNPYKFRYLRIFDYLFRFKKVNHRMHNKLIIADASIAVTGGRNISSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                 baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 YEQLHHEDHSLTEDKLYDAQSYLKELLEHNPIQWS--KAHFVADSPKK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DET---SRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 409; DB 6;
Pred. No. 1.8e-28;
                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 7685; 328pp; English
                                                              Acinetobacter baumannii protein #3559
ADA36398 standard; protein; 321 AA
                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 IVIKTNNWLNDEAAEEKTO-
                                                                                                                                                                              99US-00328352.
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34.7%;
                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100; Conservative
                                                                                                                 Acinetobacter baumannii
                                                                                 Acinetobacter baumannii
plant biocontrol agent
                                         (first
                                                                                                                                                                                                                                                               2003-576092/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                           Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     baumannii protein.
                                                                                                                                                                                                                                                                          N-PSDB; ADA32272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 321 AA;
                                                                                                                                      US6562958-B1
                                                                                                                                                                              04-JUN-1999;
                                                                                                                                                                                                   09-JUN-1998;
                                         20-NOV-2003
                                                                                                                                                          13-MAY-2003
                                                                                                                                                                                                                                             Breton G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                                                 Example;
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                    ADA36398
                                                                                                                                                                                                                                                                                                                           plants.
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The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein, useful as a vaccine for treating or infection, specifically an infection caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGKKAEOGVEVKILYDDMGSRGL------RKKGLRPFRNKGGHAEAF---FP
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VNALOLRFILDWNS----QATRDHISYDDRYFPDVNSGGTIGVQIASSGPDEE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                               Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%; Score 308; DB 6; 23.2%; Pred. No. 7.2e-19; ive 76; Mismatches 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 2112; 49pp; English.
Staphylococcus aureus protein #1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scarselli
                                                                                                                                                                                                                                                                                                                                     27-MAR-2002; 2002WO-IB002637.
                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2001; 2001GB-00007661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Staphylococcus aureus preventing Staphylococcal S. aureus, e.g. sepsis.
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                                                                                                                                                    Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Masignani V, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-120786/11.
N-PSDB; ACF73376.
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Matches 119; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR-) CHIRON SPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276
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118

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15 RESULT

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250 VRKQAYRDLHVRLQGHVVRSLQLVFLEDWL----YATSQGRAAFHGQQL----WPDDMP 300
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                                                                                                                                                                                                                                                                                                                  432
  93 IESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDSH 152
                                                                                                                                                                                                                                                                                                                                                                         477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P, Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A, Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L, Perez-Jnaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Rose M, Voss H,
                                                                          :: |:|||||| :: || || || 332 HEAKHRVWLVTPYFVPGEAARMALTSAALGGLDVRLLVP--RVSDSRLVTYAARSYFDEL
                                                                                                                                                                                                                                                                                                       EMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLOWHDPATRKTYPNEPEAKLWKR
                                                                                                                                                                                                                                                                                                                                                              153 PNIEVRLFNPFVLRKWRALGYLTDF -- PRLNRRMHNKSFTADNRATILGGRNIGDEYFKV
                                                                                                               211 GEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETS
                                                                                                                                                                     RHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDAL
                                                                                                                                                                                                                                                                                   LKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                          Listeria monocytogenes protein #2517.
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                                                                                                                                                                                                                                                                                                                                                                                                   511 IAAKILSLL 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes
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                                                                                                                            463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated nucleic acid molecule from a Xanthomonas microorganism where the nucleic acid molecule is associated with pathogenicity caused by the Xanthomonas microorganism, or its variant, that causes reduced or enhanced pathogenicity. The nucleic acid of the invention may be useful in detecting the presence of Xanthomonas bacteria in a sample, as well as in plant pathology, for example, for caused by bacterial persers. The current sequence is that of the Xanthomonas axonopodis pv. citri (Xac) plant pathology-related XAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCSSWLPPLEERTESRHFNTSKPVLLDNILQIRHTPHNNGLSDIYLLDDPHEALAARAAL 92
                                                                                                                                                                                                                                                                                                                                       axonopodis pv citri plant pathology-related XAC0014 protein.
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                                                                                                                                                                                                                                                                                                                                                                   Xanthomonas microorganism; plant; pathology; bacterial pest; Xac; Xcc;
                                                         KLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVV
                                                                                                              SVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferro JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecule from a Xanthomonas microorganism, un determining the presence of Xanthomonas bacteria in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 486;
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Laia ML, Setubal JC, Furlan LR;
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                                                                                                                                                    IESPKIAEQMERTLAD-----TTPEYAYR 479
                                                                                                                                                                              IYDQQIAKKLKQAFIDDLAVSSELTKARYAKR 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
Claim 8; SEQ ID NO 59; 145pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                            Xanthomonas axonopodis pv. citri.
                                                                                                                                                                                                                                                   ADG30702 standard; protein; 486
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                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Silva ACR, Farah
Oliveira JCF, De
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                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003089647-A1.
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                                                                                                                                                                                                                                                                                                            26-FEB-2004
                                                                                                                                                                                                                                                                                                                                        Xanthomonas
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Best Local S
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Matches
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 KAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTE 451
                                          Staphylococcus epidermidis, open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 ESFFPSKLPLINLRMNNRNHRKIVVIDGTIGYVGGFNVGDEY--IGKSKKFGYWRDTHLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 ATGSVVGEVSHDFDRYWASHSAH-NATRIIR-----SGNIGKGLQALGYNDETSRHAL
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Pred. No. 2.5e-17;
9; Mismatches 166; Indels 164; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
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ilarity 21.5%; Pre
Conservative 79;
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                                                                                                                                                                                       Staphylococcus epidermidis.
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Matches 112; Conserv
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                                                                           The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and Losynthesis and blodegradation, especially bloosynthesis of vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes. related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WiPo at the printed specification, but was obtained in electronic format directly from WiPo at the companies.
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Length 495;

391

the invention.

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The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as concoding an Staphylococcus epidermidis polypeptide with any ector; a cell comprising a recombinant expression vector of [1]; producing an S. epidermidis polypeptide, an isolated nucleic acid comprising a nucleotide sequence of at least 8 nucleotides in length; a vaccine composition for prevention or treatment of an S. epidermidis infection, comprising a nucleic acid cited above and a carrier; treating a subject for S. epidermidis infection; a recombinant or substantially pure preparation of an S. epidermidis polypeptide or its fragment; a subject for S. epidermidis infection; a recombinant or substantially coverine composition for prevention or treatment of an S. epidermidis infection; detecting the presence of a Staphylococcus mucleic acid in a sample; a computer readable medium having recorded in it the nucleotide sequence with SEQ ID NO: 1-3772 or its fragments; a computer based system for identifying fragments of the Staphylococcus genome of system for identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids; and identifying an expression modulating fragment of the Staphylococcus genome and/or plasmids; and identifying an expression modulating compositions of the present invention are useful for the diagnosis, prevention and/or treatment of an Staphylococcal epidermidis bacterial infection. This is the amino acid sequence of a S. epidermidis protein of
antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis; recombinant expression vector; infection; computer readable medium; computer based system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.
                                                              484
                                                                                                 VNAFİYDEGVARSLKQAFINDMKLSNKLİSEEYAKRNLLVK 482
                                                            MGVVIESPKIAEQMERTLAD------TTPEYAYRVTLDK
                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermis polypeptide segid 3854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; SEQ ID NO 3854; 741pp; English.
                                                                                                                                                                                                 ADS04559 standard; protein; 495 AA.
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98US-00134001.
99US-00450969.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis.
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13-AUG-1998;
29-NOV-1999;
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                                                                                                                                                  -----YNNAAF 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- DWBOI KYGYLKMI SSA----- 342
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EAGUNVYHY-------DNGF------LHSKTLVIDDEVASVGTANMDNRSFTLNFE 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P, Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
                                                                                                                                                                                                 56 VLLDNILQIRHTPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRL
                                                                                                                                                                                                                                                        223 ATGSVVGEVSHDFDRYWASHSAH-NATRIIR-----SGNIGKGLQALGYNDETSRHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MHTDPKIQAMPSETISP-----MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKP
                                                                                                                                                                                                                                                                                                  D--FP-----RINRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFA---DLDIL
                                                                                                                                                                                                                                                                                                                              ESFFPSKLPLINLRMINRNHRKIVVIDGTIGYVGGFNVGDEY--IGKSKKFGYWRDTHLR
                                                                                                                                                                                                                                                                                                                                                                                         274 IKGDAVNALQLRFILDWNSQSTRDNLTYESRYFPDVDSGGTIGIQIASSGPDE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 QPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 KAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTE
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                        10.7%; Score 291; DB 8; Length 495;
ilarity 21.5%; Pred. No. 2.5e-17;
Conservative 79; Mismatches 166; Indels 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 MGVVIESPKIAEQMERTLAD-----TTPEYAYRVTLDK
                                                                                                                                                 89 MIVDEQLEALKKQDFSKGNHQIVKFKEMVQMLL----
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                                                         Query Match
Best Local Similarity
Matches 112; Conserv
                             Sequence 495 AA;
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The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for blosynthesis and blodegradation, especially blosynthesis of Vitemain Bl.2. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 SDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNIGKGLQA---LGYNDETSRHAL---LRYRETV--EQSPLYQKIQTG-RIDWQSVQTRL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKAVYAMÓTRFIMDWNSASSTHKIDYKARYFPTFHGKGHTSMÓIVSSGPDSEWQQIKNGY 322
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                                                                                                                                                               Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 LDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 YDAMGSRTTKKSFFRTFQKNGGLVRPFFPSKLP-----LINF-RLNYRNHRKLAIIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 RATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----THLRVH
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  Amend A;
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                     Durant L;
Garrido-Garcia P, Tierrez-Martinez A, Amend A, nn E, Hain T, Berche P, Charbit A, Durant L; rro F, Garcia Del Portillo F, Gomez-Lopez N; os B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.6%; Score 287; DB 5; Length 482
25.5%; Pred. No. 5.6e-17;
ive 57; Mismatches 164; Indels
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                                                                                                                                                                                                                                               Claim 6; SEQ ID NO 2698; 192pp; French
                Chakraborty T, Domann E,
Perez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 108; Conservative
  Dominguez-Bernal G,
                                                                                                                      WPI; 2002-010914/01.
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                                                                                Voss H;
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                                                                                                                                                                                                         polypeptides
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The invention relates to identifying antimicrobial agents that target the proteins (ABB3491-1ABB3494) encoded by genes (ABA51623-ABA51634) and ABA51659-ABA51670) essential for the survival of Staphylococcus bacteria, especially Staphylococcus aurents, including antimicrobial agents that interfere with the expression of essential coding sequence products and antimicrobial agents that interfere with the function of essential coding sequence products. The genes and proteins are useful for identifying agents that decreases the growth rate of a microbe preferably S. aureus. The agents identified by the above method are bactericidal and will be useful for treating a subject infected with S. aureus or at risk of being infected by S. aureus and may be used in vaccines for producing sequence is that of a protein encoded by an essential S. aureus polynucleotide coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus; antimicrobial; growth rate; infection; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 KMANFDHF----KSLGGEVEAFFASKLPLLNFRMNRNHRKIIVIDGQLGYVGGFNIGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 BERTESRHFNTSKPVLLD-----NILQIRHTPHNNGLSDIYLLDDPHEALAARAALIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying antibacterial agents which bind to polypeptide encoded kessential coding sequences of Staphyloccus aureus, and which reduce growth rate of bacteria, by determining binding of agent to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 286.5; DB (21.1%; Pred. No. 6.4e-17. tive 86; Mismatches 16)
                                                                                                                 Staphylococcus aureus polypeptide SEQ ID NO
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                  ABB32481 standard; protein; 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 1; 67pp; English.
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                                                                                                                                                                                                  Staphylococcus aureus.
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es 106; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide from Staphylococcus aureus by contacting a polypeptide and an agent to form a mixture and determining whether the agent binds the polypeptide. The method is useful in identifying agents that bind gene products critical for the survival of microbes, preferably staphylococcus microbes, including agents that interfere with the function of such gene products. The method is used to identify new agents useful for treating or preventing bacterial infections, particularly those caused by antibiotic-resistent bacteria. This sequence represents a protein from Staphylococcus aureus of the invention.
                                                                                                                       423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying an agent that binds a polypeptide and useful for treating or preventing staphylococcal infections, comprises contacting a polypeptide and an agent to form a mixture and determining whether the agent binds
                                                              GLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQ---TRLISDTPAKGLDR
                                             DRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATD
                                                                                             VAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIF
                                                                                                           ----NSPIQIAASGPASDWHQIEYGYTKMIMSA----
                                                                                                                                              IGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADITPEYAYRVTLDKHNRLQWHDPAT
                                                                                                                                                                   VGTANMDFRSFELNFEVNAFVYDENLAKDL-------RVAYEHDITKSKQL----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to methods of identifying an agent that binds a
                                                                                                                                                                                                                                                                                                                                                                                 survival;
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                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus protein SEQ ID NO: 18.
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                                                                                                                                                                                                           KESYANRPLSVKFKESLAKLVS 490
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                                                                                                                                                                                                                                                                                 standard; protein; 493
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Best Local Similarity
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Score 286.5; DB 7; Length 493; Pred. No. 6.4e-17;

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                                                                               AEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDDNNTRGLDDLLLALDSHPNI
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                                                                                                                                                                                                                     254 EYLGLGKLGYWRDTHLRIQGDAVDALQLRFILDWNS-QAHRPQFEYDVKYFPKKNGPLG-
                                                                                                                                                                                                                                                 259 GLQALGYNDETSRHALLRYRETVEQSPLYQXIQTGRIDWQSVQ---TRLISDTPAKGLDR
                                                                                                                                                                                                                                                                     | | : | | : | | : | | ------NSPIQIAASGPASDWHQIEYGYTKMIMSA------
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    Gaps
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  141;
 Mismatches 169; Indels
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                                           Mott JE,
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 aureus polypeptide #9.

Conservative
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ARVIDSON S.
MOTT J E.
HARRIS D W.
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The invention discloses a method for identifying an agent that binds a polypeptide and an agent to form a mixture and determining whether the agent binds the polypeptide. Also claimed is a method for identifying an agent that decreases the growth rate of a microbe, making a Staphylococcus aureus with reduced virulence, which comprises altering a cading sequence in an S. aureus to introduce a mutation, a vaccine composition comprising the S. aureus organism with reduced virulence. The methods are useful for identifying an agent that binds a polypeptide, useful in treating (e.g. as a vaccine) bacterial infections, particularly those caused by antibiotic-resistant bacterial nections, particularly those caused by antibiotic-resistant bacterial of articularly bacteraemia, septic shock and serious metastatic infections virtually any organ, skin rashes, food poisoning or multisystem dysfunction, i.e. toxic shock syndrome. The inventive method identifies agent that are unrelated to existing antimicrobials and that target different aspects of staphylococcal invasion of and replication in the lost. The sequence presented is one of the S. aureus polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205
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                                                                                for treating bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVRLFNPFVLRKWRALG-----YLTDFP----RLNRRMHNKSFTADNRATILGGRNIGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRII...----RSGNIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQ---TRLISDTPAKGLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NSPIQIAASGPASDWHQIEYGYTKMIMSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KKSVYLQSPYFIPDNSYINAIKIAAKSGVDVHLMIPC--KPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 VAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                         Identification of agent that binds polypeptide, for treating bacteria infections, particularly caused by antibiotic-resistant bacteria, involves mixing polypeptide and agent, and determining whether agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5%; Score 286.5; DB 7; Length 493; 21.1%; Pred. No. 6.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNKQVQKHHDLVRMLLMDQDGFLTENNKVDHFIDGNDLYDQVLKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 169;
                                                                                                                                                                                   Example 1; SEQ ID NO 18; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKTYPNEPEAKLWKRIAAKILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KESYANRPLSVKFKESLAKLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 21.1
Matches 106; Conservative
                   2003-606127/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
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AEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLLDDNNTRGLDDLLLALDSHPNI 155
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AKEYIHLEYYTFALDGLGKRILHALEEKLKQGLEVKILYDDVGSK------NV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KMANFDHF-----KSLGGEVEAFFASKLPLLNFRMNNRNHRKIIVIDGQLGYVGGFNIGD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRII------RSGNIGK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQ---TRLISDTPAKGLDR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATD 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes isolated polynucleotides from Staphylococcus aureus comprising one of the seventeen nucleotide sequences fully disclosed in the specification. The invention is used to find agents that bind gene products critical for the survival of microbes, particularly Staphylococcus aureus and are therefore useful to treat bacterial infections particularly those caused by antibiotic-resistant bacteria. This is the amino acid sequence encoded by an unknown coding region from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NSPIQIAASGPASDWHQIEYGYTKMIMSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYLGLGKLGYWRDTHLRIQGDAVDALQLRFILDWNS-QAHRPQFEYDVKYFPKKNGPLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 EERTESRHFNISKPVLLD-----NILQIRHTPHNNGLSDIYLLDDPHEALAARAALIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVRLFNPFVLRKWRALG-----YLTDFP----RLNRRMHNKSFTADNRATILGGRNIGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Staphylococcus aureus polynucleotides useful to find agents that lgene products critical for the survival of microbes, particularly S. aureus, to treat bacterial infections particularly by antibiotic-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 493;
                                                                                                                                                           Staphylococcus aureus, microbe survival, infection, antibiotic-resistant bacteria, critical coding sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                           ŪΨ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 286.5; DB 7;
Pred. No. 6.4e-17;
5; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mott JE,
                                                                                                                                Staphylococcus aureus unknown protein #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 55; SEQ ID NO 18; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Arvidson S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Staphylococcus aureus genome
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                                ADD52524 standard; protein; 493
                                                                                                                                                                                                                                                                                                                                                                                           (PHAA ) PHARMACIA & UPJOHN CO
                                                                                                                                                                                                                                                                                                                            02-MAY-2003; 2003US-00429094.
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21.1%;
                                                                                                                                                                                                                                                                                                                                                            28-SEP-2001; 2001US-00966521.
                                                                                                                                                                                             essential coding sequence.
                                                                                               entry
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                                                                                                                                                                                                                              Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                           Quinn CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-830987/77.
                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resistant bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 493 AA;
                                                                                                                                                                                                                                                            US2003180821-A1
                                                                                                                                                                                                                                                                                             25-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                           Tomich CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96
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                                                               ADD52524;
RESULT 24
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The invention relates to identifying antimicrobial agents that target the proteins (ABB32471-ABB32494) encoded by genes (ABB51623-ABB51634 and ABB31624-ABB51670) essential for the survival of Staphylococcus bacteria, especially Staphylococcus aureus, including antimicrobial agents that interfere with the expression of essential coding sequence products and artimicrobial agents that interfere with the function of essential coding sequence products. The genes and proteins are useful for identifying agents that decreases the growth rate of a microbe preferably S, aureus. The agents identified by the above method are bactericidal and will be useful for treating a subject infected with S, aureus or at risk of being infected by S. aureus and may be used in vaccines for producing immunological response to S. aureus resulting in immunity. The present sequence is that of a protein encoded by an essential S, aureus
468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus; antimicrobial; growth rate; infection; vaccine;
                                                     VAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIF
                                                                               381 HPLVYWATFSNASDLLSSGVKIY-----TYENGF-----IHSKMCLIDDEIVS
                                                                                                                                                           VGTANMDFRSFELNFEVNAFVYDENLAKDL------RVAYEHDITKSKQL----T
                                                                                                                         IGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying antibacterial agents which bind to polypeptide encoded by essential coding sequences of Staphyloccus aureus, and which reduce growth rate of bacteria, by determining binding of agent to the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.5%; Score 286.5; DB 5; Length 502; Best Local Similarity 21.1%; Pred. No. 6.6e-17; Matches 106; Conservative 86; Mismatches 169; Indels 141; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus polypeptide SEQ ID NO 90.
                                                                                                                                                                                                                    KESYANRPLSVKFKESLAKLVS 490
                                                                                                                                                                                              RKTYPNEPEAKLWKRIAAKILS 517
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                                                                                                                                                                                                                                                                                                                    ABB32493 standard; protein; 502
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                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200177365-A2.
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                                                     376
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                                                                                                                                                                                                                                                                                                                                                       ABB32493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying an agent that binds a polypeptide and useful for treating or preventing staphylococcal infections, comprises contacting a polypeptide and an agent to form a mixture and determining whether the agent binds the polypeptide.
                EYFKVGEDTVFADLD1LATGSVVGEVSHDFDRYWASHSAHNATR11-----RSGN1GK
                                                                                                                                                                         BYLGLGKLGYWRDTHLRIQGDAVDALQLRFILDWNS-QAHRPQFEYDVKYFPKKNGPLG-
                                                                                                                                                                                                                                                                                                                                382 HPLVYWATFSNASDLLSSGVKIY------TYENGF-----IHSKMCLIDDEIVS
BERTESRHFNTSKPVLLD-----NILQIRHTPHNNGLSDIYLLDDPHEALAARALIES
                                                 AEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDSHPNI
                                                                                                    EVRLFNPFVLRKWRALG-----YLTDFP----RLNRRMHNKSFTADNRATILGGRNIGD
                                                                                                                    -----NSPIQIAASGPASDWHQIEYGYTKMIMSA-----
                                                                                                                                                                                                                                                            316 DRRKPPIAGRLODALKOPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATD
                                                                                                                                                                                                                                                                                       -----KKSVYLOSPYFIPDNSYINAIKIAAKSGVDVHLMIPC--KPD
                                                                                                                                                                                                                                                                                                              376 VAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIF
                                                                                                                                                                                                                                                                                                                                                                    IGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial; gene therapy; vaccine; diagnosis; microbial survival; gene function; bacterial infection; antibiotic-resistant bacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                       KESYANRPLSVKFKESLAKLVS 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC21402 standard; protein; 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibacterial;
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                                                                                polypeptide from Staphylococcus aurenes by contacting a polypeptide and an agent to form a mixture and determining whether the agent binds the polypeptide. The method is useful in identifying agents that bind sene products critical for the survival of microbes, preferably staphylococcus microbes, including agents that interfere with the function of such gene products. The method is used to identify new agents useful for treating or preventing bacterial infections, particularly those caused by antibiotic-resistant bacteria. This sequence represents a protein from Staphylococcus aureus of the invention when the corresponding gene is cloned into the expression vector pDE-60 or pOR-70. This encoding gene sequence corresponds to the essential gene shown in ADC21335.
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The invention discloses a method for identifying an agent that binds a polypeptide which comprises mixing a polypeptide and an agent to form a mixture and determining whether the agent binds the polypeptide. Also claimed is a method for identifying an agent that decreases the growth that comprises altering a coding sequence in an S. aureus to introduce a which comprises altering a coding sequence in an S. aureus to introduce a matation, a vaccine composition comprising the S. aureus organism with reduced virulence. The methods are useful for identifying an agent that binds a polypeptide, useful in treating (e.g. as a vaccine) bacterial infections, particularly those caused by antibiotic-resistant bacterial confidencially whose caused by antibiotic-resistant bacterial particularly bacteraemia, septic shock and serious metastatic infections or including endocarditis, arthritis, osteomyelitis, pneumonia, abscesses in virtually any organ, skin rashes, food poisoning or multisystem dysfunction, i.e. toxic shock syndrome. The inventive method identifies agents that are unrelated to existing antimicrobials and that target different aspects of staphylococcal invasion of and replication in the host. The sequence presented is one of the S. aureus polypeptides of the EYLGLGKLGYWRDTHLRIQGDAVDALQLRFILDWNS-QAHRPQFEYDVKYFPKKNGPLG- 312 GLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQ---TRLISDTPAKGLDR 315 ...-iKN 96 AEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLLDDNNTRGLDDLLLALDSHPNI EVRLFNPFVLRKWRALG-----YLTDFP----RLNRRMHNKSFTADNRATILGGRNIGD EYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRII------RSGNIGK 42 EERTESRHFNTSKPVLLD-----NILQIRHTPHNNGLSDIYLLDDPHEALAARAALIES identification of agent that binds polypeptide, for treating bacteria infections, particularly caused by antibiotic-resistant bacteria, involves mixing polypeptide and agent, and determining whether agent binds polypeptide. 10.5%; Score 286.5; DB 7; Length 502; 21.1%; Pred. No. 6.6e-17; ive 86; Mismatches 169; Indels 141; Harris DW sequence presented is one of the S. ausencoded by the essential coding region. Arvidson S, Mott JE, Example 2; SEQ ID NO 84; 122pp; English. 28-SEP-2001; 2001US-00966521 28-SEP-2001; 2001US-00966521 106, Conservative Staphylococcus aureus Quinn CL, TOMICH C C. QUINN C L. ARVIDSON S. MOTT J E. HARRIS D W. WPI; 2003-606127/57. N-PSDB; ADC25087.

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258

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AEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDSHPNI 155
                                                                                                          EYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRII------RSGNIGK
                                                                                                                                                                                                                                ||::|
-----NSPIQIAASGPASDWHQIEYGYTKMIMSA-----
                                                                                                                                                                                                                                                                                    EVRLFNPFVLRKWRALG-----YLTDFP----RLNRRMHNKSFTADNRATILGGRNIGD
                                                                                                                                                                            EYLGLGKLGYWRDTHLRIQGDAVDALOLRFILDWNS-QAHRPQFEYDVKYFPKKNGPLG-
                                                                                                                                                                                                          259 GLQALGYNDETSRHALLRYRETVEQSPLYQXIQTGRIDWQSVQ---TRLISDTPAKGLDR
                                                                                                                                                                                                                                                                    316 DRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATD
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    105 DNKQVQKHHDLVRMLLMDQDGFLTENNKVDHFIDGNDLYDQVLKD-
                                                  |: :|:|| : | :| | :: : : ::|: |::| || :: AKBYIHLEYYTFALDGLGKRILHALEEKLKQGLEVKILYDDVGSK-
                                                                                                                                                                                                                                                                                                                                                                                                                                              496 RKTYPNEPEAKLWKRIAAKILS
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N-PSDB; ACF73154.
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                                                           381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes isolated polynuclectides from Staphylococcus aureus comprising one of the seventeen nuclectide sequences fully disclosed in the specification. The invention is used to find agents the bind gene products critical for the survival of microbes, particularly Staphylococcus aureus and are therefore useful to treat bacterial infections particularly those caused by antibiotic-resistant bacteria. This is the amino acid sequence encoded by an essential coding region from the Staphylococcus aureus genome.
                                               376 VAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIF
                                                                                                      ----NSPIQIAASGPASDWHQIEYGYTKMIMSA-----
                                                                                                                                            IGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPAT
                           DRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATD
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                                                                                                                                                                                                                                                                                                                                                                                                                             survival; infection;
critical coding sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus essential protein #25
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                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus; microbe antibiotic-resistant bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus
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New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sebsis.
                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a
                                                                                      therapy; infection; sepsis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1668; 49pp; English.
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                                                               Staphylococcus aureus protein #834.
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                                                                                                                                                                                                                                                    Scarselli
ABM71594 standard; protein; 510
                                                                                      ial; vaccine; gene assay; antibiotic t
                                                                                                                                                                                                         27-MAR-2001; 2001GB-00007661
                                                                                                                                                                                    27-MAR-2002; 2002WO-IB002637
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16;

Gaps

42 EERTESRHFNTSKPVLLD-----NILQIRHTPHNNGLSDIYLLDDPHEALAARAALIES 95

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11-APR-2000; 2000FR-00004630

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nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
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                                                                                                                                                                          141;
                                                                                                                                                  DB 6; Length 510;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                   169;
                                                                                                                                                 10.5%; Score 286.5; DB 6
21.1%; Pred. No. 6.7e-17;
:ive 86; Mismatches 169
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(first entry)
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                                                                                                                                                                            Conservative
                                                                                                                                                              Similarity
                                                                                                                          Sequence 510 AA;
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16-MAY-2002
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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent electronic format directly from WIPO at the wipo.int/pub/published_lect.sequences. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LALLSGVOVKLLIPN--KPDHPLVYWATYFHAADLVKYGAKVY------TYENGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRLILED----DNNTRGLODLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGED-TVFADLDILATGSVVGEVSHDFD
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                             useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YAYRVTLDKHNRLOWHDPATRKTYPNEPEAKLWKRIAAKILS 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Obs. 10.4%; Score 282.5; DB 5; Local Similarity 22.5%; Pred. No. 1.4e-16; les 104; Conservative 76; Mismatches 167;
                                                      SD;
                                                       Ehrlich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 VKLLIDAWGSNKTK-----MSNFKELQ-
                                                                                                                                                       Claim 6; SEQ ID NO 978; 2504pp; French
                         (INRG ) INRA INST NAT RECH AGRONOMIQUE
                                                      Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; protein; 420
                                                                                                               New nucleotide sequence use
lactis and related species.
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                                                      Sorokine
                                                                                  WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                           Sequence 480 AA;
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                                                       Bolotine A,
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The invention relates to a substantially purified nucleic acid molecule encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a recombinant DNA construct for expression of a nitrite reductase gene in a plant cell, and a plant cell comprising the recombinant DNA construct. The nucleic acid is useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest. Sequences given in records for SEQ 105 9692-16825 represent a group of 7134 Mxyococcus xanthus proteins and peptides. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVLLDNILQIRHTPHNNGL---SDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 VGELFGQALAEAAERGVHVKVLYDAVGSWTSRRSFFAGLRARGVD------IR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFAD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 AFKPFSLS--RGLRHLL-----RKDHRKILVVDGEVAFTGGVNISAHWAPAEMGAAWRD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 LDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYR 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVLRIEGPAVHELERCFSATW------RMMFQGRF-------HRLTRRL 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGVSGGLLTRYYLPRRHGVVQGNACQLLRDGVEAYPAMLEAIRGARRYVRMETYMFVSDA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKG-----LDRDRRKPPIAGRLQDALKQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 EKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKA
                                                                                                                                                                                                                                                                                                                                                               New substantially purified Myxococcus xanthus nucleic acid molecule encoding a nitrite reductase, useful for determining gene expression, identifying mutations in a gene of interest, and for constructing mutations in a gene of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 275; DB 9; Length 420;
; Pred. No. 5.7e-16;
65; Mismatches 179; Indels 128; Gaps
                                    DNA replication; gene regulation; gene expression.
                                                                                                                                                                                                                                                                                              Wiegand RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 16463; 25pp; English.
seq id 16463
                                                                                                                                                                                                                                                                                          Slater SC,
                                                                                                                                                                                                                                                      (MONS ) MONSANTO TECHNOLOGY LLC
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M. xanthus protein sequence,
                                                                                                                                                                                                                    10-JUL-2000; 2000US-0217883P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.1%;
                                                                                                                                                                                 10-JUL-2001; 2001US-00902540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 23.55
Matches 114; Conservative
                                                                                                                                                                                                                                                                                          Hinkle GJ,
                                                                                                                                                                                                                                                                                                                               WPI; 2005-028716/03.
                                                                        Myxococcus xanthus
                                    Transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 420 AA;
                                                                                                         US6833447-B1
                                                                                                                                             21-DEC-2004.
                                                                                                                                                                                                                                                                                          Goldman BS,
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This sequence is a Helicobacter pylori protein of unspecified function.

The protein may be used in a vaccine to prevent or treat H. pylori

The protein may be used in a vaccine to prevent or treat H. pylori

The protein or to identify H. pylori polypeptide binding compounds, useful

as potential H. pylori life cycle activators or inhibitors. The DNA and

probes derived from it may be used for the identification of H. pylori infection. Nucleic acid

a sample, and the diagnosis of H. pylori infection. Nucleic acid

sequences complementary to the DNA act as antisense sequences, and can be

used to prevent the translation of H. pylori mRNA. Antibodies against the

sprotein can be used in immunoassays to evaluate the abundance and

distribution of H. pylori-specific antigens. The genomic sequence of H.

Cylori (ATCC 55679) was determined from overlapping contigs generated by

mechanically shearing the bacterial DNA. The sequences were analysed for

mechanically shearing the bacterial DNA. The sequences were analysed for

CRF of at least 180 nucleotides, and the predicted coding regions defined

Cy computer evaluation. To identify likely H. pylori antigens for vaccine

development, the amino acid sequences predicted from various ORF were

CC analysed for significant homology to other known or exported membrane

Cy poteins. Having identified and determined the sequences of interest,

particular regions can be isolated from H. pylori by PCR amplification

cy for recombinant polypeptide production, e.g. in E. coli hosts
                      ----RPLWOKLLE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis;
| | | | : | | | : | 369 AVFADPRLGQQLEDSFRGDCGD-CREVTLAEFRR-
                                                                                                                                                                                                                                                                                                                  H. pylori ORF 05cp11911orf35 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 492; 1145pp; English.
                                                                                                                                                                                                AAW55249 standard; protein; 206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-00625811.
96US-00758731.
96US-00736905.
96US-00738859.
96US-00761318.
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                                                                                                                                                                                                                                                                          (first entry)
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| RALSLL 416
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                                                                                                                                                                                                                                                                            26-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-1996;
28-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                     bacterium
                                                         514
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                                                                                                                                                                                                                                     AAW55249;
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10.1%; Score 274.5; DB 2; Length 206;

Query Match

454 VVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAA 513

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us-10-665-990a-14.rag

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                                                                                                                           ilarity 23.2%; Pre
Conservative 73;
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98US-0094190P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                              Query Match
Best Local Similarity
Matches 118; Conserv
                                                                                         Sequence 490 AA;
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27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms; for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorphisms encoded by the genes are used for detection/identification of the genes are used for detection/identification of arry a gene-containing vector are used to select compounds that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, animals or microorganisms other than P. luminescens and are able to alter response or sensitivity to toxins and antibiotics produced by P. luminescens. Cells transformed to express the genes are useful for recombinant production of the proteins, particularly toxins and antibacterials useful as insecticides, bactericides and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful
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                                       380
                                                                                         440
                                                                                                                                          LDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPATRKTY- 499
                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague;
                                      321 PIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVH
                                                     SGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFN
                                                                                                       GAWERYRNKLVRMGANVYEIRNDFFNRQIKGR---FSTKHSLHGKTIVFDDALTLLGSFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence of Photorhabdus luminescens and encoded polypeptides, useful e.g. as therapeutic antimicrobials and agricultural pesticides.
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Danchin A;
              11;
 2.1e-16;
ches 84; Indels
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                                                                                                                                                                                                                                                                                                                                                             Photorhabdus luminescens protein sequence #2117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Frangeul L,
 Pred. No. 2.1e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 2117; 1205pp; French.
                                                                                                                                                                                           ---PNEPEAKLWKRIAAKILSLLP 520
                                                                                                                                                                                                                   IHEKNSPDTSFFLRLIKEWSKVLP 202
                                                                                                                                                                                                                                                                                   ABM69020 standard; protein; 490 AA
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              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECH SCI.
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31.4%;
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              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Photorhabdus luminescens.
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(CNRS ) CNRS CENT NAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-148459/14.
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            whooping cough.
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              64;
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             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCSSWLPPLEERTESRH-FNTSKPVLLDNILQIRHTPHNNGL-----SDIYLLDDPHEAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.1%; Score 274.5; DB 6; 23.2%; Pred. No. 8e-16; ive 73; Mismatches 185;
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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular tragets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as templates for antibacterial drugs, including anti-P. aeruginosa-derived peptides or polypeptides, as target production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa caused infection, and in detection of P. aeruginosa sequences of Pseudomonas species using biochip technology. Sequences ABO67826-CRB084196 represent P. aeruginosa charpeptides of the invention. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 WRPWVEEALAARQVSGYKG--LKALVRMTRTPTLANN---RVRLLVNGEASFEAMFKAIS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLLDDNNTRGLDDLLLALDSHPN 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 VQMHGFS-----TGSGMLNRF-QVNFRNHRKVVVVDGECGFVGGHNVGVEY--LGEKP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 SRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 WLPPLEERTESRHFNTSKPVLLDNILQIRHTP--HNNGLSDIYLLDDPHEALAARAALIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 AARQVILVÕFFIVRDDALGORLOOLLLERAANGVEVFFLYDAIGSHALPHRYVERLRQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 IEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 VFA---DLDILATGSVVGEVSHDF--DRYWASHSAHNATRIIRSGNIGKGLQALGYNDET
                                                                                                       3acterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 PLAPWRDTHMELRGPAVACLQESFAEDWYWATHSL------
                                                                                                                                                                                                                                                                                                                                                                    Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.9%; Score 268; DB 7;
24.5%; Pred. No. 4.1e-15;
iive 60; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 17125; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Deloughery C,
                                                                       aeruginosa polypeptide #554.
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                                                                                                                                                                                                                                                                                                98US-0094190P
                                                                                                                                                                                                                                                                                                                                                                Nolling J,
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 24.5
Matches 111; Conservative
                                                                                                                                         Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                    2003-615309/58.
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                                                                                                                                                                                                                                                                                                                                                                Rubenfield MJ,
                                                                                                                                                                                                                                            8-FEB-1999;
                                                                                                                                                                                                                                                                                                27-JUL-1998;
                                       29-JUL-2004
                                                                         Pseudomonas
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     AB068379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTESRHFNTSKPVL---LDNILQIRHTPHNNGLSDIYLLDDPHEALAARAALIESAEHSL 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RRADLHFAVSGPVFPWRSDN----RFALLNDGVRFF-----PRMLLA-----IEAAQRSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDSHPNIEVRLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPFVLRKWRALG---YLTDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFK-VGEDTVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 ADLDILATGSVVGEVSHDFDRYWASHSAHNA------TRIIRSGNIGKGLQALGYND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETSRHALLRYRETVEOSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IWLATPYFLPTWKVRRALRKAAQRGVEVRLLLAG-RLTDHAPVRYAGQRYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 KPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 ELELYLVEDGHCAELFLVALLDARRRGVAVRCLFDGFGCLGLGSAWIQRLREAGGELRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 DALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----BROHRDILOSLVRALNGSRRR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 109; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7; Length 584;
                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
9.9%; Score 268.5; DB 7;
Best Local Similarity 24.2%; Pred. No. 3.8e-15;
Matches 107; Conservative 59; Mismatches 167;
                                     Bush
                                                                                                                                                                                   Disclosure, SEQ ID NO 24311; 455pp; English.
                                   Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:||::::| ||
PRLLRAGVRIHEYQPRF-------
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(GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABO68379 standard; protein; 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNTEMGVVIESPKIAEQMERTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FNLDANLEALDPDFTNEAAASL
                                 Nolling J,
                                                                 WPI; 2003-615309/58.
N-PSDB; ABD09136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 584 AA;
                                Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
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ID ABO68
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Length 579; Indels

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                                                                                                                                                                                                                                                                                                                                                                     The invention describes an isolated nucleic acid comprising a nucleotide sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO: 13772) and encoding an Staphylococcus epidermidis polypeptide with any of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as given in the specification. Also described are: a recombinant expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis; recombinant expression vector; infection; computer readable medium;
:: | |: |: | :: | :: | 374 LAIPC--KPDHPFVYWATFSNAADLLDSGVNIYTYQNGF---------IHSK
                                                      186 NKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAH
                                                                                                                          246 NATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLI
                                                                                                                                                              -------DKGNAAIQIA
                                                                                                                                                                                                 306 SDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVT
                                                                                                                                                                                                                                                                    366 VLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAK
                                                                                                                                                                                                                                                                                                                                           426 TFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKH
                                                                                     235 RKIIIIDGQIGYVGGFNVGDDYLGLGKLGYWRDTHTRVQGECIDALQLRFILDWNSQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polypeptide and encoding nucleic acid derived from Staphylococcus epidermidis, useful for diagnosing, preventing and/or treating an S. epidermidis bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermis polypeptide seqid 4379.
                                                                                                                                                                                                                                                                                                                                                                                                                517
                                                                                                                                                                                                                                                                                                                                                                                                                                                   491
                                                                                                                                                                                                                                                                                                                                                                                                                                      NRLQWHDPATRKTYPNEPEAKLWKRIAAKILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; SEQ ID NO 4379; 741pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADS05084 standard; protein; 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0064964P.
98US-00134001.
99US-00450969.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        computer based system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004-580138/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Doucette-Stamm L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADS01312
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                  DVGSK-
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29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-NOV-2004
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                    193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 DNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTD--FP-----RLNRRMH 185
                                       LKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKP 389
                                                                                                                                             523
                                                                                                                                                                                                                                                                                                                                                                                                                                                 epidermidis; open reading frame; ORF; bacterial infection; gene therapy.
   --FVEM 422
                                                           IYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%; Score 259.5; DB 5; 22.3%; Pred. No. 1.9e-14; ive 70; Mismatches 178;
                                                                                                                                                                                475
                                                                                                                                                                                                         --PPLILPPQYDSEGALCQVVASGPADAQETCSLF--
                                                                                                                                                                                TEMGVVIESPKIAEQMERTL -----ADTTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 4176; 267pp; English.
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                                                                                                                                                                                                                                                                                                         ABP39331 standard; protein; 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0055779P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epidermidis.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1997;
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                                       330
                                                                      423
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Acinetobacter baumannii.

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                                                                                                                                                                                                                                                                                                                                                                                            186 NKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAH 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------HRPQFKFDQKYFPKKNG--DKGNAAIQIA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMIPC---KPDHPFVYWATFSNAADLLDSGVNIYTYQNGF-------IHSK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKH 485
                                                                                                                                                                                                                                                                                                                                                                 76 IYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLLD
                                                                                                                                                                                                                                                                                                                              IDLFTDGHKLYEKVLEDIYNAODYIHLEYYTFELDGLGKRILDALETKLKEGLEVKLLYD
                                                                                                                                                                                                                                                                                                                                                   DNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTD--FP-----RLNRRMH
                                                                                                                                                                                                                                                                                                                                                                                                                                      246 NATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 VLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAK
                                                                                                                                                                                                                                                                                                                                                                                                           235 RKIIIDGQIGYVGGFNVGDDYLGLGKLGYWRDTHTRVQGECIDALQLRFILDWNSQS--
                                                                                                                                                                                                                                                             'Match 9.5%; Score 259.5; DB 8; Length 494; Local Similarity 22.3%; Pred. No. 1.9e-14; Indels 103; Gaps les 101; Conservative 70; Mismatches 178; Indels 103; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486 NRLOWHDPATRKTYPNEPEAKLWKRIAAKILS 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLL-----TKEVYDKRPLSIKFKEGLAKLIS 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA36341 standard; protein; 166 AA
                                                                                                                                                                                                                                                                                    Matches 101; Conservative
                                                                                                                                                                                                                                           Sequence 494 AA;
                                                                                                                                                                                                                     the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306
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New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for

(GENO-) GENOME THERAPEUTICS CORP

ä

Bush

Breton G,

WPI; 2003-576092/54,

N-PSDB; ADA32215

98US-0088701P. 99US-00328352

04-JUN-1999; 09-JUN-1998;

13-MAY-2003

Example; SEQ ID NO 7628; 328pp; English.

plants.

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67 DVDGK-VFIGSFNFDPRSTYLNTEVGLVIESSQLQTQISVMLDQHLPQVAYQLKLNSQGQ 125
                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane construction and membrane transport protein, petroleum spill, hydrocarbon degradation, gram positive aerobic bacterium, marker, identification, microorganism, fine chemical production; transformation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 GYVKYRKPLLKAGIKLYELQP------NHAVPATKDKGLTGSSVTSLHAKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 IVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum; brevibacterium lactofermentum; MCT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.3%; Score 252; DB 6; Length 166;
larity 37.3%; Pred. No. 1.7e-14;
Conservative 26; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOWHDPATRK---TYPNEPEAKLWKRIAAKILSLLPIEGLL 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum MCT protein SEQ ID NO:78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genetic engineering
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB76548 standard; protein; 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 166 AA;
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Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;

plant biocontrol agent.

Acinetobacter baumannii protein #3502.

(first entry)

20-NOV-2003

ADA36341;

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RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacteium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 294-296; 1119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schroeder H,
                                                 99US-0141031P.
99DE-01031454.
99DE-01031478.
99DE-01031563.
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99DE-01032128.
99DE-01032180.
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99DE-01042088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 422 AA;
                              23-JUN-2000;
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09-JUL-19
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These
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                                                                                                                                                                                                                                                      PTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHA 405
                                                                                                                                                                                                                                                                                                            -----LHTKYMIADPDDTTGNEALGVLGSSNLDIRSFGLNYEISLMIAK 375
                                               -----DNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRAL 171
               92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene. measuring soversair of
---RRFRRPDLRNHRRWLIIDGHTAFMGSQNLIAPSYLQKKNIKLGRE---WKDLMVELTG
                                                                                                           172 GYLTDFPRLNRRMHNKSFTADNRATILGGRN-IGDEY-----FKVGEDTVFADLDILATG
                                                                                                                                                                      226 SVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  410
                                                                                                                                                                                                                                                                                                                                                                                                                  459 PKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPATRKTY 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; SEQ ID NO 6514; 246pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                       GNLIHEL-NALTDRYRTVSFKLTLDKWNQRSW-----RRRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
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                                                                            93 GVKVRLLFDHVGSWKYPGYHRLKKELNRMGFAWYLM-
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2000JP-00159162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2001 (first entry)
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07-APR-2000;
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Query Match 9.3%; Score 252; DB 4; Length 422; Best Local Similarity 23.4%; Pred. No. 7.4e-14; Matches 108; Conservative 58; Mismatches 179; Indels 116; Gaps

are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lyaine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office 8888888888888888

Sequence 500 AA;

67 TPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAER 126 127 GVRVRLLLD------DINITRGLDDLLLALDSHPNIEVRLFNPFVLRKWRAL 171 171 GVKVRLLFDHVGSWKYPGYHRLKKELNRMGFAWYLM-------LPLQPWR-- 213 172 GYLTDFPRLNRRMHNKSFTADNRATILGGRN-IGDEY----FKVGEDTVFADLDILATG 225 214 ---RRFRRPDLRNHRKMLIIDGHTAFMGSQNLIAPSYLQKKQNIKLGRE--WKDLMVELTG 268 226 SVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSP 285 269 PIVSSMEMIFAGDWYVESN------EALDIRDHAEAHGYIGNTQKDSATN 312 346 PTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHA 405 | : | : | : | : | : | | : | 352 PDESLLEAVTSACYRGVTVELFVS--EQADQFAIDHAQSSYYQALLEAGVKIYQF-PKPD 408 VPATKDKGLTGSSVTSLHAKTFIVD----GKRIF--IGSFNLDPRSARLNTEMGVVIES 458 286 LYOKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFV 345 313 LVQLIPSG------PGYTTEPNLR-----MFNSIVHHAKERLILCSPYFI 351 V------LHTKYMIADPDDTTGNEALGVLGSSNLDIRSFGLNYEISLMIAK 453 Query Match 9.3%; Score 252; DB 4; Length 500; Best Local Similarity 23.4%; Pred. No. 9.7e-14; Matches 108; Conservative 58; Mismatches 179; Indels 116; Gaps PKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPATRKTY 499 GNLIHEL-NALTDRYRTVSFKLTLDKWNQRSW----RRRY 488 459 409 ઠે 8 g ò ò g g ò ò 요 ò g ð g Š

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Sequence 2405, Ap
Sequence 23909, A
Sequence 5559, Ap
Sequence 5591, Ap
Sequence 7685, Ap
Sequence 2733, Ap
Sequence 22, Appl
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1 MHTDPKIQAMPSETISPMKT......KLWKRIAAKILSLLPIEGLL
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Maximum DB
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Sequence 2405, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
FOR INAMATION:
FILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATY
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFRENCE: 2709-2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2405

LENGTH: 543
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                      2, Appli
9934, Ap
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16500, A
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             US-09-141-206-2

US-09-949-016-934

US-09-949-016-934

US-09-948-0394-11632

US-08-968-758-6

US-09-908-758-6

US-09-902-540-1650

US-09-902-540-1650

US-09-902-540-1650

US-09-902-540-16817

US-09-902-540-14817

US-09-107-149-2

US-09-128-352-334

US-09-38-352-358

US-09-38-352-358

US-09-38-352-4
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US-09-540-236-2405
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: GTC99-03P4
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5559
LENGTH: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5591
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501 QLALEGMAPSVSYQVRIDRSGSRPKLVWIDERDGRPQVLRHEP-GSLWRRLNAWVAGMIG 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 RIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDA
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41.0%; Pred. No. 2.1e-39;
ive 51; Mismatches 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.1%; Score 493.5; DB 2;
.larity 43.8%; Pred. No. 6.3e-41;
Conservative 47; Mismatches 73;
                                                                                                                                                                      ; Sequence 5559, Application US/09328352; Patent No. 6562958
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US-09-328-352-5591
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US-09-328-352-5559
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Best Local Similarity 41.0%
Matches 100; Conservative
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                                                                            560 LEKML 564
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US-09-328-352-5591
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Sequence 23909, Application US/09252991A

Patent No. 6521795

GENERAL INFORMATION:
APPLICANT MACC J. RUbenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PRILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23909

LENGTH: 564
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                       | :|| :|| : ||||| :|: |||| || :|- GSGFHLLGASEDAFVARAALIRAAQRSLDIQYYIVHDGLTTRALAYELLKAADRGV 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 HNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGV
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                                                                            473 TPEYAYRVTLDKHNRLQWHDPATRKTYPN-----EPEAKLWKRIAAKILSLLPIEGL
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US-09-252-991A-23909
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Best Local Similarity 36.7<sup>1</sup>
Matches 200; Conservative
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US-09-252-991A-23909
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                                                                                                                                                                                                                                                                                                                                                                                          LFNLMYLAAERGVRVRLLLLDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLT 175
                                                                                                                                                                                                                                                                                                                     ------YNNAAF 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||: :|
BAGVNVYHY------DNGF-----LHSKTLVIDDEVASVGTANMDNRSFTLNFE 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 LRYRETVEQSPLYQKIQTGRIDWQSVQ---TRLISDTPAKGLDRDRRKPPIAGRLQDALK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 QPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLL 391
                                                                                                                                                                                                                                                                          1 MHTDPKIQAMPSETISP-----MKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKP
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                                                                                                                                                                                       Length 495;
                                                                                                                                                                                  10.7%; Score 291; DB 2; Length 49 ilarity 21.5%; Pred. No. 4e-20; Conservative 79; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452 MGVVIESPKIAEQMERTLAD-----TTPEYAYRVTLDK 484
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APPLICANT: The Pharmacia & Upjohn Company
ITILE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS;
FILE REPERENCE: 268.6212010;
CURRENT APPLICATION NUMBER: US/09/828,523A
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/266,327
PRIOR FILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNAFIYDEGVARSLKQAFINDMKLSNKLTSEEYAKRNLLVK
                                                                                                                                                                                                                                                                                                                     89 MIVDEQLEALKKQDFSKGNHQIVKFKEMVQMLL-----
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                                                                                                                  ORGANISM: Staphylococcus epidermidis US-09-134-001C-4273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // Sequence 22, Application US/09828523A
// Patent No. 6764823
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           PRIOR FILING DATE: 1997-08-14
                             NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4273
LENGTH: 495
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                                                                                                                                                                                                       Best Local Similarity
Matches 112; Conserv
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TYPE: PRT
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE DE INVENTION:
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                        US-09-328-352-7685

Sequence 7685, Application US/09328352

Sequence 7685, Application US/09328352

Patent No. 6562958

APPLICANT: No. 6562958

TITLE OF INVENTION: BUCHEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERBNCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILLING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7685

LENGTH: 221
212 TIHHTWDENLNKYAYKLKLDPNNHIYWQQETPKGPVIYKKEPEMKWWQKAGMKLLSWLPL 271
                                                                    AVPATKDK-GLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAE 463
                                                                                                                                                         QMERTLADTTPEYAYRVTLDKHNRLQWHD--PATRKTYPNEPEAKLWKRIAAKILSLLPI 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 LLCSCSSWL--PPLEERTESRHFNTSKPVLLDNILQIRHTPHNNGLSDIYLLDDPHEALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.0%; Score 409; DB 2; Length 32 34.7%; Pred. No. 2.6e-32; ive 44; Mismatches 110; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Acinetobacter baumannii
US-09-328-352-7685
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Matches 100; Conservative
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	RESULT 9  US-09-902-540-16463  i Sequence 16463, Application US/09902540  j Batent No. 683347  GENERAL INFORMATION: APPLICANT: Goldman, Barry S. APPLICANT: Hinkle, Gregory J. APPLICANT: Hinkle, Steven C. TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B CURRENT APPLICATION NUMBER: 60/217,883  FILE REFERENCE: 2001-07-10 PRIOR APPLICATION NUMBER: 60/217,883  FILE REFERENCE: 2001-07-10  MUMBER OF SEQ ID NOS: 16825  SEQ ID NO 16463  LENGRANISM: Myxococcus xanthus US-09-902-540-16463	Query Match 10.1%; Score 275; DB 2; Length 420; Best Local Similarity 23.5%; Pred. No. 1.2e-18; Matches 114; Conservative 65; Mismatches 179; Indels 128; Gaps 15; Qy 55 PVLLDNILQIRHTPHNNGLSDIYLLDDPHBALAARAALIESAEHSLDLQYYIMRNDI 111 Db 38 PGVSGGLLTRYYLPRRGVVQGNACQLLRDGVEAYPAMLEAIRGARRYVRETYMFVSDA 97  Qy 112 SGRLLFNLMYLAARGVVRTRLLLDDNNTRGLDDLLLALDSHPNIEVR 158  Qy 112 HIII	LY DAVGSWTSRRSFFAGLRANG LARRMHNKSFTADNRATILGGR LAST AND LAST ASHS AND ATRILY STATE ASHS AND ATRILY ASHS AND ASS AND AS
Qy 42 EERTESRHFNTSKPVLLDNILQIRHTPHNNGLSDIYLLDDPHEALAARAALIES 95  104 DNKQVQKHHDLYRALLMQDGFLTENKVDHFIDGNLVKDIKN 151  Qy 96 AEHSLDLQYYIMRNDISGRLLFNLMYLAAERGWRVLLLDDNNTRGLDDLLLALDSHPNI 155  152 AKEYIHLEYYTFALDGLGKRILHALEEKLKQGLEVKILYDDNGSKNN 198  Qy 156 EVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGD 205  159 KWANFDPF	Qy 436 IGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPAT 495	SOFTWARE: Patentin version 3.1 SEQ ID NO 90 LENGTH: 502 TYPE: PRT ORGANISM: Artificial Sequence FRATURE: COTHER INFORMATION: expression in E. coli. US-09-828-523A-90	Query Match Best Local Similarity 21.1%; Pred. No. 1.2e-19; Matches 106; Conservative 86; Mismatches 169; Indels 141; Gaps 16;  Qy 42 EERTESRHFNTSKPVLLDNILQIRHTPHNNGLSDIYLLDDPHEALAARAALIES 95 ::   : :

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US-09-252-991A-17125

1 Sequence 17125, Application US/09252991A

1 Sequence 17125, Application US/09252991A

2 Patent No. 6551795

3 GENERAL INFORMATION:

3 TITLE OF INVENTION:

4 TITLE OF INVENTION:

5 TITLE OF INVENTION:

5 TITLE OF INVENTION:

6 CURRENT APPLICATION NUMBER: US/09/252,991A

7 CURRENT PILING DATE: 1999-02-18

7 PRIOR APPLICATION NUMBER: US 60/074,788

7 PRIOR PELICATION NUMBER: US 60/094,190

7 PRIOR APPLICATION NUMBER: US 60/094,190

7 PRIOR SPELICATION NUMBER: US 60/094,190

7 PRIOR APPLICATION NUMBER: US 60/094,190

7 PRIOR SPELING DATE: 1998-07-27

8 PRIOR FILING DATE: 1998-07-27

8 PRIOR FILING DATE: 1998-07-27

8 PRIOR FILING DATE: 1998-07-27

9 PRIOR FILING DATE: 1998-07-27

9 PRIOR FILING DATE: 1998-07-27

9 PRIOR FILING DATE: 1998-07-27

9 PRIOR APPLICATION NUMBER: US 60/094,190

9 PRIOR APPLICATION NUMBER: US 60/094,190
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Patent No. 6380370

APPLICANT: Lyun Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 VQMHGFS-----TGSGMLNRF-QVNFRNHRKVVVVDGECGFVGGHNVGVEY--LGEKP 350
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17125
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APPLICANT: MACC J. Rubenfield et al.
APPLICANT: MACC J. Rubenfield et al.
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2 4311
LENGTH: 584
                                                                                                                                                                                                        AVFADPRIGGQUEDSFRGDCGD-CREVTLAEFRR-------RPLWQKLLE 410
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------ARQHRDILQSLVRALNGSRRR------- 426
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                 EKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKA
                                      GIKLYELOPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMG
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Patent No. 6551795
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Best Local Similarity 24.2%
Matches 107; Conservative
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US-09-252-991A-24311
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13 GVRQYRVEMLKSGIELYEFKPVLERRRTWYEIVTGSVIPA-----KGKNKSSLHAKFF
                                                                 428 IVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNR
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APPLICANT: Kr"ger, Burkhard
APPLICANT: Sch"der, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
                                                                                                                                                                                                                                      488 LQWHDPATRK---TYPNEPEAKLWKRIAAKILSLLPIEGLL 525
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CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT APPLICATION NUMBER: US/06.23
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-26
PRIOR FILING DATE: 1999-07-08
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Sequence 7628, Application US/09328352
Sequence 7628, Application US/09328352
Sequence 7628, Application US/09328352
GENERAL INFORMATION:
APPLICANT: Gary L. Brecon et al.
APPLICANT: Gary L. Brecon et al.
TITLE OF INVENTION: BAUNANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 TFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKH 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 ILMIDDEISSIGSANMDFRSFELNFEVNAFIYDEDIÅKQLRQ------AFEKDIEQS 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 494;
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llarity 37.3%; Pred. No. 5.3e-17;
Conservative 26; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.5%; Score 259.5; DB 2; Best Local Similarity 22.3%; Pred. No. 5.9e-17; Matches 101; Conservative 70; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486 NRLOWHDPATRKTYPNEPEAKLWKRIAAKILS 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466 KLL-----TKEVYDKRPLSIKFKEGLAKLIS 491
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR LILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4176
                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 GYVKYRKPLLKAGIKLYELOP---
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US-09-328-352-7628
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Best Local Similarity
Matches 60; Conserv
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Sequence 4117, Application US/09543681A
Fatent No. 6605709
GENERAL INPORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
FRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4717
             APPLICANT: NAMPOOTHIRI, Madhavan
TITLE OF INVENTION: No. 6562607el Nucleotide Sequences Coding for the cls Gene
FILE REFERENCE: 032301 WD 1919
CURRENT APPLICATION NUMBER: US/09/848,726
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 GVKVRLLFDHVGSWKYPGYHRLKKELNRMGFAWYLM------LPLQPWR-- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 TGGNNG-----FYSDYRESLKRMTAAIDEAEEYIYVEIYIMAWDSYTQPFFAALERAHNR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVRVRLLLD-------DNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRAL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 PIVSSMEMIFAGDWYVESN-------EALDIRDHAEAHGYIGNTQKDSATN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 LYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFV 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 PIKSGIDALAKLVQDGIDVTVLINSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 LVQLIPSG------PGYTTEPNLR-----MFNSIVHHAKERLILCSPYFI 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPATKDKGLTGSSVTSLHAKTFIVD-----GKRIF--IGSFNLDPRSARLNTEMGVVIES 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 ---RRFRRPDLRNHRKMLIIDGHTAFMGSQNLIAPSYLQKKNIKLGRE--WKDLMVELTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :| :|:||:||:|:|
352 PDESLLEAVTSACYRGVTVELFVS--EQADQFAIDHAQSSYYQALLEAGVKIYQF-PKPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 TPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAER
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al Similarity 23.4%; Score 252; DB 2; Length 500;
al Similarity 23.4%; Pred. No. 3.4e-16;
108; Conservative 58; Mismatches 179; Indels 116;
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23.3%; Pred. No. 1.4e-15;
ive 84; Mismatches 163; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      459 PKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPATRKTY 499
                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-848-726-2
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; ORGANISM: Proteus mirabilis
US-09-543-681A-4717
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Best Local Similarity 23.3
Matches 112; Conservative
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Best Local S:
Matches 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 GYLTDFPRLNRRMHNKSFTADNRATILGGRN-IGDEY----FKVGEDTVFADLDILATG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSP 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 TGGNNG----FYSDYRESLKRMTAAIDEAEEYIYVEIYIMAWDSYTQPFFAALERAHNR 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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PRIOR APPLICATION NUMBER: DE 19940766.5
PRIOR FILING DATE: 1999-08-27
PRIOR PLILING DATE: 1999-08-27
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US-09-602-787A-78
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US-09-848-726-2
Sequence 2, Application US/09848726
Patent No. 6562607
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 78
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Gaps

314

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246 NATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLI 305
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                                                                                                                                                                                                                                                                                                         EKSUYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKA 393
                                                                                                                                                                                                                                                                                                                                                                                                                              394 GIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMG 453
118 LKKNGGFVQTFITSQKALLKF-RLNYHDHRKIVVIDGKVGYIGGFNVADQY--AGTTKKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1000, Application US/09710279
Fatent No. 6703492
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P103480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
PRIOR PLING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
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                                                               ADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLO---ALGYNDETSRHA
                                                                                                                                                                                 274 LERYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQP
                                                                                                                                                                                                                                                                                                                                                               257 KKRVWIOTPYLVPDDSVLAALKVAAASGVDVKIMIP--DKPDHPFIYRATQYYGRLLMKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 DVGSK-------KVRLSK---FKHFRALGGEVEAFFPSKVPLINFRMINRNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 RKIIIIDGQIGYVGGFNVGDDYLGLGKLGYWRDTHTRVQGECIDALQLRFILDWNSQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 IYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 442;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    454 VVIESPKIAEQME-----RTLADTTPE 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| :|:| :|:| 388 AVLYDKKIIDQLEAIFLEDRKKCTTMTPE 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (442)
; OTHER INFORMATION: variable amino acid
US-09-710-279-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-710-279-1000
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LENGTH: 442
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER FILING DATE: 1997-08-15
SPOFTWARE: Patentin version 3.1
SEQ ID NOS: 6812
SECTION 10 2064
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                                                                                                                                                                                       DL-----LLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRAT 196
                                                                                                                                                                                                                                                                                                                   197 ILGGRNIGD-EYFK----VGEDTVFADLDILATGSV----VGEVSHDFDRYWASHSAHNAT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                     258 YTGSMNWVDPRYFKQDAGVGQ---WIDIMVRMEGPVSTTLG-IIYAFD--WEMETGERHL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312 PPPPDNNIMPFEQANGHT------TQVIASGPGFPE-----ELIQQSLIT-- 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAKGLDRDRRKRPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------AIYSARKELVMTTPYFVPSDDLAHAISTAAMRGVDVSIIV 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 NSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFI 428
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                                                                                                                                                    AARAALIESAEHSLDLQYYIWRNDISGRLLFNL---MYLAAERGVRVRLLLDDNNTRGLD 143
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23.8%; Pred. No. 3.1e-15;
ive 60; Mismatches 188; Indels
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Matches 107; Conservative
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		RESULT 20 US-09-22-991A-24635  US-09-22-991A-24635  Facent No. 6521795  Fatent No. 6521795  Fatent No. 6521795  FATEN CONTRAPTION:  MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOM  TITLE OF INVENTION:  MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOM  TITLE OF INVENTION:  CURRENT APPLICATION NUMBER: US/09/252,991A  CURRENT FILING DATE: 1999-02-18  PRIOR FILING DATE: 1998-02-18  PRIOR FILING DATE: 1998-02-18  FRIOR SEDILON NUMBER: US 60/094,190  PRIOR FILING DATE: 1998-07-27  NUMBER OF SEQ ID NOS: 33142  FAMOR APPLICATION NUMBER: US 60/094,190  PRIOR SEQ ID NOS: 33142	1domonas aeruginosa  8.4%; Score 228; DB 2; Length 800;  1arity 23.2%; Pred. No. 1.9e-13;  Conservative 61; Mismatches 186; Indels 94; Gaps  NGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIMRDISGRLLFNLMYLAABERG      :	188 188 184 204 305 305 365 422
Qy 366 VLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAK 425 ::       :	RESULT 19 US-09-107-532A-4088 ; Sequence 4088, Application US/09107532A ; Patent No. 6583275 ; GENERAL INFORMATION: APPLICANT: Lynn A Doucette-Stamm and David Bush TITLE OF INVENTION: WCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF SEQUENCES: 7310 CORRESPONDENCE ADDRESS:	ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham STRATE: Massachusetts COUNTRY: USA ZIP: 0.2354 COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM ISO9660 COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: PC COMPUTER: DC COMPUTER: DC COMPUTER: DC COMPUTER: DC COMPUTER: DC COMPUTER: DC COMPUTER: DC COMPUTER: DC COMPUTER: DC COMPUTER: DC COMPUTER: DC COMPUTER: DC COMPUTER: US/09/107,532A FILING DATE: 14 May 1998 FILING DATE: 14 May 1998 FILING DATE: 14 May 1998 FILING DATE: July 2. 1997	ATTORNEY/AGENT INFORMATION:  NAME: ATTAINSION, Pamela Deneke REGISTRATION NUMBER: 40, 489 REFERENCE/DOCKET NUMBER: GTC-012 RELECOMUNICATION INFORMATION: TELEPHONE: (781)893-8277 INFORMATION FOR SEQ ID NO. 4088: SEQUENCE CHARACTERISTICS: LENGTH: 386 amino acids TYPE: amino acids TYPE: amino acids TOPOULGY: linear MOLECULE TYPE: protein HYPOPHITICAL: YES ORIGINAL SOURCE:	PEATURE:  NAME/KEY: misc feature  CORGANISM: Enterococcus faecium  NAME/KEY: misc feature  LOCATION: (B) LoCATION 1386  SEQUENCE DESCRIPTION: SEQ ID NO: 4088:  US-09-107-532A-4088  Query Match  B.5%; Score 231.5; DB 2; Length 386;  Best Local Similarity 23.3%; Pred. No. 2.5e-14;  Matches 97; Conservative 66; Mismatches 174; Indels 79; Gaps 14;  Matches 97; Conservative 66; Mismatches 174; Indels 79; Gaps 14;  Oy 58 LDNILQIRHTPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIMRNDISGRLLF 117  Db 2 LATYLKICPAPQTR-MNCYTLLTDGQEKLDSLLQDLKKAKGHSIHIEYXAFVTDNIGQQVL 60  OY 118 NLMYLAABRGVRVRLLLDDNNTRGLDDLLLALDSHPNIEVTRRWFALGYLTDF 177  :::

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FERENTAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITILE OF INVENTION: BYTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITILE OF INVENTION: BYTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION OF SEQ 10 NOS: 6812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 LISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGID 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 VTVLTNSLQATDVAAVHSGYVKYRK------PLLKAGIKLYELQPNHAVPATKDK 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 GLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVI-ESP---KIAEQMERT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 TRIIRSGNI----GKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEY-----FKVGEDTVFADLDILATGSVV------GEVSHDFDRYWASHSAHNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 IESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLLDDNNTRGLDDLLLALDSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ::| | | ::| | | 370 VRIIT------PYIPDKKFIQLVTRGAYPDLLSAGVRIYEYSPGF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 469 LADITPEYAYRVILDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLL 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 FADSOEVYPHSI-----KTSWYQ-------KLVKEIAQLFAPIL 491
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
8.1%; Score 219; DB 2; Length 491;
Best Local Similarity 21.4%; Pred. No. 6.8e-13;
Matches 101; Conservative 61; Mismatches 139; Indels 170;
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR PELLING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1998-05-12
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 4158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 3595, Application US/09134000C; Patent No. 6617156
                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pneumoniae US-09-583-110-4158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 NHSİPSDGLTIPYĞSĞ-----
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; ORGANISM: Enterococcus faecalis
US-09-134-000C-3595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin version 3.1
SEQ ID NO 3595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-134-000C-3595
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Patent No. 6699703
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT:

APPLICANT:

Gary Breton et. al

TITLE OF INVENTION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION:

PREDAMCE:

Z109.2004001

CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT FILING DATE:

PRIOR APPLICATION NUMBER:

WUMBER OF SEQ ID NOS:

14342

SEQ ID NO 10241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 MHNKSFTADNRATILGGRNIGD-EYFK----VGEDTVFADLDILATGSVVGEVSHDFDRY 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 SVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 ------GPPEDL----IHQALLTAAYAAKEHLIMTTPYFVPSDDLLHAICTAA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSS 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAY 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LHTKSVLVDGELSLVGTVNLDMRSLWLNFEITLVIDDAGFGSD----LAAVQDDYIS 470
     LHGKVAVIDDDWSTIGSSNLDPLSLSLNLEANLVIRDVAFNGQLYQHLRELARRHCRRIS 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 LDD-NNTRGLDDLLLALDSHPNIEV-----RLFNPFVLRKWRALGYLTDFPRLNRR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 SDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 QHRKMVMIDNYIAYTGSMNWVDPRYFKQDSGVGQ---WIDLMARMEGPVATSMGIVYSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.1%; Score 220; DB 2; Length 501; Best Local Similarity 23.0%; Pred. No. 5.6e-13; Matches 105; Conservative 63; Mismatches 177; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVTLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKI 515
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                                                                                                                                                                                                                                         Sequence 10241, Application US/09489039A
Patent No. 6610836
                                                                                                         410 -RRHARRGYWWRAPA---DFPRLP 429
                                                       LDKHNR--LOWHDPATRKTYPNEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                             RESULT 21
US-09-489-039A-10241
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US-09-583-110-4158
     350
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                              313 ---LDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTN 369
                                                                 202 FVWRDNQDHRDDİERHYLKMLTSARREVIIANAYFFPGYRLLHAMRNAARRGVRVKLIVQ 261
                                                                                                                                                                                                 430 DGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQ 489
                                                                                                                                                                                                                                    303 DDHWATVGSSNLDPLSLSLNLBANLITHDRVFNQTLRDNLNGLIARDCQRIDKTMLPKRN 362
                                                                                                                                                           ----PLHGKVALA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                               370 SLOATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                  490 W--------HDPA-------TRKTYPNEPEAKLWKRI 511
                                                                                                                                                                                                                                                                                                                262 G--EPDIPIVKFGAHLLYHYLVKGGVQIYEYRRR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US, 94107,433
FILING DATE: 30-Unn-1998
PRIOR APPLICATION NUMBER: 60,085131
APPLICATION NUMBER: 60,085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60,051553
ATTORNEY, AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE//DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LÕCATION 1...518
SEQUENCE DESCRIPTION: SEQ ID NO: 3177:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3177, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 518 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3177:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02354
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US-09-107-433-3177
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APPLICANT:

APPLICANT:

GATY Breton et. al

TITLE OF INVENTION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION:

PREMOMOTABE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE:

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR PLING DATE:

1999-01-29

NUMBER OF SEQ ID NOS:

14342

SEQ ID NO 12789
                                                                      13;
                                                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                              211 DMIRK------TRLMYHLHRKIVVIDGKIGWTGGFNVGDQYLNVTEKFGYWRDTHİ 260
                                                                                                                                                                                          YIWRNDISGRLLFNLMYLAAERGVRVRLLLDDDNNTRGLDDLLLA--LDSHPNIEVRLFNP 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                      341
                                                                                                                                                                                                                                                                                                                                                              LATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETV 281
                                                                                                                                                                                                                                                                                                                                                                                                      261 RIVGTAVFSLOEIFIMDW-----NA------SVKYPEER-----MTYHEKY 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 FKLPEDHEV-----EHLSLQVVSDGP-----DSEEEILKSGFVRMIFSAEKSVWIQT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQ 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 TILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 IGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKG--- 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
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                                                                                                                                                                                                                               151 YAFFNDTIGNOFLDVLIEKLHEGVEVYLIYDPWGSPGANKKFFARYVDAGGKVAPFITSR
                                                                                                                                                                                                                                                                           FVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGED-TVFADLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                             EQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 IYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLLD
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                                                                      Gaps
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                                                                      96;
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7.9%; Score 216; DB 2; Length 415; larity 22.4%; Pred. No. 1e-12; Conservative 62: Mismatch...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | | : | : | : | : | | : | AFVGGINYSAEHMSDYGPEAKQDYAVKVEGPVVLDIL-QFE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.9%; Score 215.5; DB 2; 21.4%; Pred. No. 1.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402 PNHAVPATKDKGLTGSSVTSLHAKTFIVD 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----IYDSGF-----IHAKIMVID 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12789, Application US/09489039A
Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 100; Conservative
                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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US-09-489-039A-12789
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                          Query Match
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Sequence 13301, Application US/09902540
; Patent No. 6833447
; GENREAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; TILLE REFERENCE: 38-10(15849) B.
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT PILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13301
                                                                                        247
                                                                                                                                      428
                                                                                                                                                                    429 VDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRL 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 RILLEGGVRIWEYE------LSMWHSKTWLVDDSLSVVGSTNWDPLALTT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 NTEMGVVIESPKIAEQM----ERTLADTTPEYAYRVTLDKHNR-LQWHDPATRKTYPNEP 503
                                                                                                                                                                                                                                                                             -----WLDKHLR- 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- 201
                                         309 PAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLT
                                                                                     ------RYLQAIDGAEHEVVLAHAYFLPDKGFMRALKRASRRGVTVRLML
                                                                                                                                    369 NSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 QSPLYQKIQTG-RIDWQSVQTRLI--SDTPAKGLDRDRRKPPIAGR----LQDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                              Query Match 5.5%; Score 149; DB 2; Best Local Similarity 21.9%; Pred. No. 1.8e-06; Matches 54; Conservative 46; Mismatches 81;
189 KLFLSGFAG------GHRL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-438-185A-437; Sequence 437, Application US/09438185A; Patent No. 6822071; GRNERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 LEECSVVVEDVALAAQLAASFEKDL
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                                                                                                                                                                                                                                                                                                                                                                        -----GSRRVY 340
                                                                                                                                                                                                                                                                                                                            489 QWHDPATRKTY 499
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US-09-902-540-13301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 213
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Facent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: Mycococcus xanthus Genome Sequences and Uses Thereof;

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

FRIOR FILING DATE: 2000-07-10

FRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825
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                                                                                          153 P----NIEVRLFNPFVLRKWRALGYLTDFPRL----NRRMHNKSFTADNRATILGGRNIG 204
                                                                                                                                    231 RLRQLGIEAHKFNKVI-------PRLTVAYNNRDHRKILIVDGQIAYTGGVNLA 277
                                                                                                                                                                                     DEY-----FKVGEDTVFADLDILATGSVV-------GEVSHDFDRYWASHSAHNA 247
                                                                                                                                                                                                                     248 TRIIRSGNI----GKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTR 303
                                                                                                                                                                                                                                                                                                             304 LISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGID 363
                                                                                                                                                                                                                                                                                                                                                                                                                       -----INOATESVYITTPYLIIDYDLTETIKNAAMRGVD 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 VTVLTNSLQATDVAAVHSGYVKYRK------PLLKAGIKLYELQPNHAVPATKDK 412
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1ESAEHSLDLQYY1WRND1SGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDSH
                          76 IYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLD
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7.6%; Score 208; DB 2; Length 378;
Best Local Similarity 22.5%; Pred. No. 5.6e-12;
Matches 97; Conservative 47; Mismatches 163; Indels 124;
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US-09-902-540-11860
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Sequence 9934, Application US/09949016
; Sequence 9934, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANTY VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: LOGO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOCTHARE: PSECE for Windows Version 4.0
; SEQ ID NO 9934
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                                                                                                                                                                                                                                                                                                 289 LILKCSSYRQARWWAQEITELAQGPG------RNFLQLHRHDSYAPPRPGNLARWFV 339
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                                                                                                                                                                                                                                                                                                                                                                                                                              340 NGASYFÀAVADAILRAQEEIFITDWWLSPEVYLKRPAHSDD-----WRLDI------MF
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                                                                                                 5.2%; Score 141.5; DB 2; Length 933;
18.5%; Pred. No. 0.00013;
tive 87; Mismatches 182; Indels 265;
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                                                                                                                                                                     Conservative
                                                                                                                               Similarity
          ; ORGANISM: Human
US-09-141-206-2
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                    APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REPERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR PILING DATE: 1998-11-12
PRIOR PILING DATE: 1998-104-08
NUMBER OF SEQ ID NOS: 1074-08
SQOTWARR: FastSEQ for Windows Version 3.0
SEQ ID NOS: PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT PARENT P
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Sequence 2, Application US/09141206

Patent NO. 6.18759:
GENERAL INFORMATION:
APPLICANT: Steed, Paul M.
APPLICANT: Lasala, Daniel J.
TITLE OF INVENTION: Amino Acid Sequence of Hum:
Patent No. 6187559
FILE REPERENCE: 4-30148/P1/CGC1954/R
CURRENT PILING DATE: 1998-08-27
BARLIER APPLICATION NUMBER: 60/057,802
BARLIER FILING DATE: 1997-08-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
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Kalman, Sue
Davis, Ronald
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US-09-438-185A-437
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LENGTH: 933
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Best Local Simi
Matches 121;
US-09-141-206-6
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                                                                                                                                                                                                                      349 ADAILRAQ-----EEIFITDWWLSP-EVYLKRPA-----HSDD-----WRLDI--- 385
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                                                                                                                                                                                                                                                                                                                     165 LRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGG---------RNIGD----
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                                                                                            257;
                                                            Length 933;
                                                           Query Match 5.0%; Score 135.5; DB 2; Length Best Local Similarity 18.9%; Pred. No. 0.0005; Matches 123; Conservative 92; Mismatches 179; Indels
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US-99-141-206-6
; Sequence 6, Application US/09141206
; Sequence 6, Application US/09141206
; Patent No. 6187559
; GENERAL INFORMATION:
; APPLICANT: Steed, Paul M.
; APPLICANT: Lacala, Daniel J.
; TITLE OF INVENTION: Amino Acid Sequence of Human PLD2A; Patent No. 6187559
; FILE REFERENCE: 4-30148/PL/CGC1954/R
; CURRENT APPLICATION NUMBER: US/09/141,206
; CURRENT APPLICATION NUMBER: 06/057,802
; EARLIER PILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 6
; LENGTH: 922
                                                                                                                           -----RHFNTSKP
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                                                                                                                           30 LLCSCSS-----WLPPLEERTES--
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ORGANISM: Human
             Human
           ) ORGANISM: Huma:
US-09-949-016-9934
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GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION:

PREPRINCE:

CURRENT APPLICATION NUMBER: US,09/489,039A

CURRENT FILING DATE:

PRIOR PLILING DATE:

1999-01-29

NUMBER OF SEQ ID NOS:

14342

SEQ ID NO 11632
                                                                                                                                                                                                                                                                                                           162
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                                                                                                                                        ----MFKRKABEGVRVSILL-----FKELELALGINSGYSKRALMLLHPNIKV-MRHP 433
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480 ESAASQPPTPRPDSPATPDLSHNQFFWLGKDYSNLITKDWVQLDRPFEDFIDRETTPRMP 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 LDNILQIRHTPHNNGLSDIYLLD---DPHEALAARAALIESAEHSLDLQYYIWRNDISGR 114
                                                                                                                                                                                                                                        115 LLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALD------SHPNIEVRLFNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         540 WRDVGVVVHGLPARDLARHFIQRW-----NFTKTTKA------KYKTPTYPYLLP
                                                                                                                                                                                                                                                                                                                                                                                                                   -----RNIGD--
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4.9%; Score 134; DB 2; Length 922;
18.4%; Pred. No. 0.0007;
cive 84; Mismatches 173; Indels 2
                                                                                                     30 LLCSCSS-----WLPPLEERTES------RHFNTSKP--
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Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                FVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGG
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Patent No. 6610836
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11632
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                                                     Conservative
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Best Local Similarity
                          Similarity
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377 HSDD-----WRLDI------MLKRKAEEGVRVSILLFKE-----VELALGINSGYSKRT 419
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                                                                                                                                                                                                                                                                          98 HSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDS----- 151
                                                                                                                                                                                                                                                                                                                                                       ----HPNIBVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIG--- 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPEKSVYLVSPYFVPTKSGTDALAKLVQDGID------VTVLT-----368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                    80; Mismatches 165; Indels 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                    --DEYFK---VGEDTVFADLDILATGS---VVGEVSHD---
                                                                                                                                                                                               Score 133.5; DB Pred. No. 0.0008
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DNA Sequences
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APPLICANT: Frohman, Michael A.
APPLICANT: Morris, Andrew
TITLE OF INVENTION: No. 6379665e
TITLE OF INVENTION: DNA Sequence.
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: 3031 Research Drive
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; Sequence 6, Application US/09536224
; Patent No. 6379665
                                                                                                                                                                                                 4.9%;
                      TELEFAX: 510-222-9758
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             Query Match
Best Local Similarity 18.6'
Matches 101; Conservative
                                                                              LENGTH: 932 amino acids
                                                                                                                                     MOLECULE TYPE: protein US-08-968-7528-6
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ZIP: 94806
COMPUTER READABLE FORM:
                                                                                                  amino acid
                                                                                                                     linear
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STATE: Californ
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  TELEPHONE:
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                                    54 KPVLLDNILQIRHTPH-----NNGLSDIYLLDDPHEALAARAALIESAEHSLD----L 102
                                                                                                               OYYIWRNDISGRLLFNLMYLAAER--GVRVRLLLD------DINYTRGLDDLLLA 148
                                                                                                                                                                                                                  208 FKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNI------ 256
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                                                                        RTVMLSKFKRNKHOOHLAQLPKLSQSVDDVEFFYAPAE---FREALLTRIAHATQRICII 61
                                                                                                                                                                                                                                                                                                                                                                             198 LVQGRGVNRLDRPDRPRSPEIKNDIRQYRQELRDRS-YHFVGTAGDEELSV-----TP
                                                                                                                                                                                           LDSHPNIEVRLFN-PFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 SLQATDVAAVHSGYVKYRKP--LLKAGIKLYELQPNHAVPATKDKGLTGSSV-----
Mismatches 199; Indels 133; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08968752B
Patent No. 6643073
GENERAL INFORMATION:
GENERAL INFORMATION: Michael A.
APPLICANT: Frohman, Michael A.
APPLICANT: Morris, Andrew
TITLE OF INVENTION: No. 6643073el Phospholipase D Polypeptide and
TITLE OF INVENTION: DNA Sequences
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476 YAYRVTLDKHNRLQWHDPATRKTYPNEPEAKLWKRI 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, VACURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,752B
FILING DATE: 13-AUG-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Giotta, Gregory J.
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: ONYX2004
TELECOMMUNICATION INFORMATION:
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SYSTEM: PC-DOS/MS-DOS
  81;
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CITY: Richmond
STATE: California
COUNTRY: USA
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APPLICATION NUMBER: US 6(
FILING DATE: 05-SEP-1996
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::|:::||: | | | | :::|
632 BSQHFLYIENQPFISCSDGRTVLANKVGDBIVDRILKAHEQGQCFRVYLLLPLLPGFBGDI 691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | : | : | : | : | : | | 692 STGGGNSIQ----AILHFTYRTLCRGEHSILHRLKAAMGTAWRDYMSICGLRTHGELGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 ----HPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | :: :|:: ||: 465 WDDVQYRLTDLGDPSEPVHLQTPTLGSDPAATPDLSHNQFFWLGKDYSNLITKDWVQLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        748 PI-----SELIYIHSKMLIADDRTVIIGSANINDRSLLGKRDSELAILIKD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 HSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 --DEYFK---VGEDTVFADLDILATGS---VVGEVSHD-----
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,224
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.9%; Score 133.5; DB 2; Best Local Similarity 18.6%; Pred. No. 0.0008; Matches 101; Conservative 80; Mismatches 165;
                                                                                                                                                                                                                                   ONYX2004
                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/968,752
                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory J.
REGISTRATION NUMBER: 32,028
REFERENCE/DOCKET NUMBER: ONYXZ
TELECOMUNICATION INFORMATION:
TELEPHONE: 510-222-9700
TELEFAX: 510-222-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NSLQATDVAAVHSGY----
                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 932 amino acids
| TYPE: amino acid
| TYPE: amino acid
| MOLECULE TYPE: protein
| WG-09-536-224-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   586 TSTANOLPF--TLPGGOC--TTVQV-----LRSVDRWS-----AGTLENSILNAYLHT 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 LKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGID-------VTVLT----- 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NSLQATDVAAVHSGY--------VKYRKPLLKAGIKLYELQP 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISTGGGNSIQ----AILHFTYRTLCRGEYSILHRLKAAMGTAWRDYISICGLRTHGELG 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 NHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRS--ARLNTEMGVVIE--- 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   458 -SPKI----AEQMERTLADTTPEYAYRVTLDKHNR--LQWHDPATRKTYPNEPEAKLWKRI 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 VTLW-------AHHEKLLVVDQVVAFLGGLDLAYGRWDDLHYRLTDLGDSSES 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 LILKCSSYRQARWWAQEITELAQGPGRDFLQLHRHDSYAPPRPGTLARWFVNGAGYFAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 LDNILQIRHTPHNNGLSDIYLLD---DPHEALAARAALIESAEHSLDLQYYIWRNDISGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
4.9%; Score 133.5; DB 2; Length 933;
Best Local Similarity 18.3%; Pred. No. 0.0008;
Matches 121; Conservative 88; Mismatches 175; Indels 277;
                                                                            APPLICANT: LOUNG, David W.
APPLICANT: Tompkins, Christopher K.
TILE OF INVENTION: PHOSPHATIDYLCHOLINE PHOSPHOLIPASE D
FILE REFERENCE: 077319/0144
CURRENT APPLICATION NUMBER: US/09/107,149
CURRENT FILING DATE: 1996-106-30
EARLIER APPLICATION NUMBER: 08/768,147
EARLIER FILING DATE: 1996-12-17
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 LLCSCSS-----WLPPLEERTES------RHFNTSKP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: :: | :: | :: | 542 DVGVVVHGLPARDLARHFIQRW-----NFTKTTKA-----
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Sequence 17, Application US/09107149
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-09-107-149-17
                             Patent No. 6274363
GENERAL INFORMATION:
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RESULT

RESULT 35 US-09-107-149-17

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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                    199 LQSDAIQRL---DSEERVRCAEIKNCIRQFRFNLRTHDGYDIKGNASNNQLTVTPLVGLG 255
                                                                                                                                                                                                                                                                                                                           313 DF-----YIPPEEPFKIIGALPYLYEINLRKFTQRFQRFIDNDQLTVRLWKDGDNT--- 363
                                                                     158 SGASİNNVYLH------KLD------KYRYDRYHIIHNAELANTMKQFİVDSL 198
                                                                                                                                                                                                     315 RDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQAT 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT FILING NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14817
LENGTH: 155
                           199 GGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATR----IIRSG
                                                                                                                                                                                                                                   255 NIGKGLOALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLD
                                                                                                                                                                                                                                                                                             375 DVAAVHSGYVKYRKP--LLKAGIKLYEL------QPNHAVPATKDKGLTGSS
                                                                                                                                                                                                                                                                                                                                                                                                              419 VISLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESP--KIAEQMERTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.5%; Score 123; DB 2; Length 155; 30.2%; Pred. No. 0.00044; Live 17; Mismatches 63; Indels
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14817, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-107-532A-5960
; Sequence 5960, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
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Best Local Similarity
Matches 38; Conserv
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US-09-902-540-14817
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Batent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BEETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR PELING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 SVQTRLISDIPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 QDGIDVTVL---TNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLT 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 SRHFNISKPVLLDNILQIRHTPH-----NNGLSDIYLLDDPHEALAARAAL---IESA 96
                                                                                                   APPLICANT: Hinkle, Cargory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wigger C.
TITLE OF INVENTION: Wyxcoccuus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 16500
LENGTH: 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 GSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HTKLMVVDGVWSLIGSANWDPRSLRLNFEFNVECYDTALAMQLEGVVA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.8%; Score 130; DB 2; Length 459; larity 20.7%; Pred. No. 0.00054; Conservative 70; Mismatches 196; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.8%; Score 130.5; DB 28.0%; Pred. No. 0.0002; iive 22; Mismatches 77
                Sequence 16500, Application US/09902540 Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 EHSLDLQYYIWRNDISGRLLFNLMYLA
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Myxococcus xanthus US-09-902-540-16500
                                                       GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 49; Conserv
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US-09-902-540-16500
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LENGTH: 459
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Best Local S
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ORGANISM: Homo sapiens
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US-09-107-149-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 AGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEM 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.5%; Score 122; DB 2; Length 183; larity 21.3%; Pred. No. 0.00074; Conservative 39; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09107149

Patent No. 6274363

GENERAL INCRAMION:
APPLICANT: Lengt, David W.
APPLICANT: Tompkins, Christopher K.
TITLE OF INVENTION: PHOSPHATIDYLCHOLINE PHOSPHOLIPASE D.
TITLE REFERENCE: 077319/0148

CURRENT APPLICATION NUMBER: US/09/107,149

CURRENT APPLICATION NUMBER: 08/768,147

EARLIER APPLICATION NUMBER: 08/768,147

SARILER PILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 2

LENGTH: 933
                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...183
SEQUENCE DESCRIPTION: SEQ ID NO: 5960:
                                                                                                                                                                                                                                                                          NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REBERBNCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecium
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                         OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 183 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5960:
SEQUENCE CHARACTERISTICS:
            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
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Matches 36; Conserv
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                                                                                                                             386 ----MLKRKAEEGVRVSILLFKE----VELALGINSGYSKKALMLLHPNIKV-MRHPDQ 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 PATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRS--ARLNTEMGVVIE----SPK 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : :|: | | | : : | | | : : | | | 30 ------SELIYIHSKVLIADDRTVIIDSANINDRSLLGKRDSELAVLIEDTETEPS 799
                                                                                                                                                                                                                                                                                       115 LLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDS------HPNIEVRLFNPFV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                 436 VILW-------AHHEKLLVVDQVVAFLGGLDLAYGRWDDLHYRLTDLGDSSES 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I---AEQMERTLADTTPEYAYRVTLDKHNR--LQWHDPATRKTYPNEPEAKLWKRIA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 LDNILQIRHTPHNNGLSDIYLLD---DPHEALAARAALIESAEHSLDLQYYIWRNDISGR
                                                                                                                                                                                                                                                                                                                                                                                      -----RNIGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 RETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 LKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGID-------VTVLTNSLQATD-
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Length 933;
                                               Indels
                                                                                               30 LLCSCSS-----WLPPLEERTES------RHFNTSKP-
4.5%; Score 121.5; DB 2;
18.0%; Pred. No. 0.013;
tive 88; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                      165 LRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGG----
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                                                  Conservative
                    Best Local Similarity
Matches 118; Conserval
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Search completed: May 2, 2006, 06:14:55 Job time : 50 secs

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(without alignments)
1321.448 Million cell updates/sec
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2720
1 MHTDPKIQAMPSETISPMKT......KLWKRIAAKILSLLPIEGLL 525
                                                                                                        2, 2006, 06:24:35 ; Search time 166 Seconds
GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Published Applications AA Main:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*

3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*

1: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Database

	Description	-14 Sequence 14, App]	16.	8 Sequence 18,		4 Sequence 4,	20 Sequence 20,	Sequence 908	Sequence	Seguence 356,		9 Seguence 59,	3854	Sequence 22, A	Sequence 18,	B Sequence	90,	Sequence 84,	===	083 Sequence 9083	4379,	78, Ar	Sequence 2, A	6514,	equence 8	225.		Semiono 3177
SUMMARIES	ΩI .	US-10-665-990A	US-10-665-990A	90A	US-10-066-551-4	US-10-665-990A-	US-10-665-990A-	US-10-335-977-9085	~	-881-7	776	US-10-418-861B-5	US-10-724-972A-	US-09-828-523A-2	US-09-966-521-18	US-10-429-094-1	-828-523A	US-09-966-521-8	US-10-429-094-8	US-10-335-977-9	24	US-10-627-476-7	US-09-848-726-2	526-	US-10-156-761-8	US-10-474-776-2	US-10-472-928-2	US-10-617-320-3
	Match Length DB	525 5	525 5	525 5	525 4	525 5	525 5	502 4	502 4	428 3	224 4	486 4	495 4	493 3	493 3	493 4	502 3	502 3	502 4	206 4	494 4	422 4	500 3	500 3	404 4	510 4	510 5	518 5
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	Score	2720	2712	2708	2643	2643	2643	632	632	590	359	296	291	286.5	286.5	286.5	286.5	286.5	286.5	274.5	259.5	252	252	252	226	219	219	215
Result	No.	-	7	c	4	2	9	7	80	თ	10	11	12	13	14	15	16	17		19								

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2384, Ap 2386, Ap 2388, Ap	2390, Ap 2392, Ap 31511, A	354, App 75, Appl 6, Appli	79, Appl 2203, Ap 215690,	22273, A 7642, Ap 120957,	175603, 2316, Ap
Sequence Sequence Sequence	Sequence Sequence Sequence			Sequence Sequence Sequence	Sequence Sequence
US-10-501-282-2384 US-10-501-282-2386 US-10-501-282-2388	US-10-501-282-2390 US-10-501-282-2392 US-10-450-763-31511 US-10-450-763-31510	US-10-474-792-354 US-10-312-273-75 US-10-137-129A-6	US-10-498-327-79 US-10-408-765A-2203 US-10-424-599-215690	US-10-369-493-22273 US-10-032-585-7642 US-10-437-963-120957	US-10-437-963-175603 US-11-097-143-2316
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3 5 8 3 6 8	3 3 3 1 3 3 3 1 3 4 3 3 1	35 36 37	8 8 8 8 8 6 0 4	4 4 4 1 2 6	4 4 5

## ALIGNMENTS

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Sequence 14, Application US/1066590A

Sequence 14, Application US/2004025322A1

GENERAL INFORMATION:

APPLICANT: Apicella, Michael A.

APPLICANT: Apicella, Michael A.

APPLICANT: Apicella, Michael A.

TITLE OF INVENTION: Vaccine and compositions for the prevention and treatment of Nei

TITLE OF INVENTION: 108-ctions

FILE REFERENCE: 17023-031001

CURRENT APPLICATION NUMBER: US/10/665,990A

CURRENT FILING DATE: 2003-09-19

PRIOR FILING DATE: 2003-09-19

PRIOR FILING DATE: 2003-01-31

PRIOR PELICATION NUMBER: US 60/344,452

PRIOR PELICATION NUMBER: US 60/310,356

PRIOR APPLICATION NUMBER: US 60/310,356

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-08-06

PRIOR PELING DATE: 2001-01-31

NUMBER OF SEQ ID NOS: 32

SOFTWARE FEASESQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ILQIRHTPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLAAERGVRVRLLLDDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Neisseria gonorrhoeae 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-665-990A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 14
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SHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLY OTRLISDSPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPI OTRLISDSPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPI OTRLISDSPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPI GIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPHAVF GIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPHAVF GIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPHAVF GIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPHAVF SIHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMER SIHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMER TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 5 TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 5 TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 5 TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 5 TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 5 TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 5 TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 5 TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 5 TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 5 TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 5 TLOM NUMBER: US 10/65,990A TLOGATON NUMBER: US 10/621,184 GDATE: 2001-01-31 GDATE: 2001-01-31 GDATE: 2001-01-31 GASTE: 2001-01-31 GASTE: 2001-01-31 GASTE: 2001-01-31 GASTE: 2001-01-31 GASTE: 2001-01-31 GASTE: 2001-01-31 GASTE: 2001-01-31 GASTE: 2001-01-01-01-01-01-01-01-01-01-01-01-01-	Matches 522; Conservative 99.4%; Score 2.706; Us 3; Lengin 523; Beet Local Similarity 99.4%; Pred; No. 4.1e-232; Matches 522; Conservative 1; Mismatches 2; Indels 0; Gaps Matches 510; Conservative 1; Mismatches 2; Indels 0; Gaps Matches 522; Conservative 1; Mismatches 2; Indels 0; Gaps Matches 522; Conservative 1; Mismatches 2; Indels 0; Gaps Matches 522; Conservative 1; Mismatches 2; Indels 0; Gaps Matches 522; Conservative 1; Mismatches 2; Indels 0; Gaps Matches 522; Conservative 1; Mismatches 2; Indels 0; Gaps Matches 522; Conservative 1; Mismatches 2;	DD 1 MHTDPKIQAMPSETISPWKTRSLISLICLILCSCSSWLPPLEERTESRHFNTSKPVLLDN 60  Qy 61 ILOIRHTPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYWRNDISGRLLFNLM 120	121	Db 181 NRAMHNKSFTADNRATILGGRNIGDEYFKYGEDTYFADLDILATGSVVGEVSHDFDRYWA 240 Qy 241 SHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSV 300 Db 241 SHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPFYQKIQTGRIDWQSV 300
AHNATRIIRSGNIGKGLOALGYNDETSRHALLRYRETVEOSPLYGKIGTGRIDWGSV 300 AHNATRIIRSGNIGKGLOALGYNDETSRHALLRYRETVEOSPLYGKIGTGRIDWGSV 300 AHNATRIIRSGNIGKGLOALGYNDETSRHALLRYRETVEOSPLYGKIGTGRIDWGSV 300 LISDTPPAKGLDRDRRKPPIAGRICOALKQPEKSYLVSPYPUTKGGTDALAKLVOD 360 LISDTPAKGLDRDRRKPPIAGRICOALKQPEKSYLVSPYPUTKGGTDALAKLVOD 360 LISDTPAKGLDRDRRKPPIAGRICOALKQPEKSYLVSPYPUTKGGTDALAKLVOD 360 LISDTPAKGLDRDRRKPPIAGRICAGIKLYELQPHHAVPATKOGTGTGSSYT 420 LISDTPAKGLDRDRRKPPIAGRICAGIKLYELQPHHAVPATKOGTGTGSSYT 420 WTVLTNSLOATDVAAVHSGYVKYRKPLLKAGIKLYELQPHHAVPATKOKGTGTGSSYT 420 WTVLTNSLOATDVAAVHSGYVKYRKPLLKAGIKLYELQPHHAVPATKOKGTGTGSSYT 420 WTVLTNSLOATDVAAVHSGYVKYRKPLLKAGIKLYELQPHHAVPATKOKGTGTGSSYT 420 WTVLTNSLOATDVAAVHSGYVKYRKPLLKAGIKLYELQPHHAVPATKOKGTGTGSSYT 420 WTVLTNSLOATDVAAVHSGYVKYRKPLLKAGIKLYELGPEGL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 KHNRLCMHDRER: US 60/310,136 ATTON: VARCHERE: US 60/310,356 ATTON: VARCHERE: US 60/216,070 ATTON: VARCHERE: US 60/	-10-665-990A-16 Query Match Query Matches 523; Core 2712; DB 5; Length 525; Best Local Similarity 99.6%; Pred. No. 1.8e-222; Matches 523; Conservative 1; Mismatches 1; Indels 0; Gaps	Qy         1 MHTDPKIQAMPSETISPMKTRSLISLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDN 60           I	꿈〓꿈	Qy         181 NRRWHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWA 240           Db         181 NRRWHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWA 240           Qy         241 SHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSV 300

Neis

QTR.LISDTPAKGLDRDRRKEPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQD	361
361 GIDVTVLTNSLQATDVAAVHSGYVKYRRPLLKAGIKLYELQPNHAVPATKDKGLTGSSVT 420 	Qy 421 SLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRV 480 
421 SLHAKTFIVDCKRIFIGSFNLDPRSARLNTEWGVVIESPKIAEQMERTLADTTPEXAYRV 480 	Qy 481 TLDKHNRLQWHDPATRKTYPNBPEAKLWKRIAAKILSLLPIEGLL 525    -
481 TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525 	RESULT 5 US-10-65-990A-4 . Semience 4. Application US/10665990A
US-10-066-551-4 US-10-066-551-4 ; Sequence 4, Application US/10066551 ; Publication No. US20030100071A1 ; GENERAL INFORMATION: ; APPLICANT: Apicella, M. A. ; APPLICANT: Edwards, J. L. ; APPLICANT: Gibson, B. W. ; APPLICANT: Scheffler, K.	Publica GENERAL APPLIC APPLIC TITLE TITLE FILE F CURREN CURREN
# APPLICANT: BLOWN, E. TITLE OF INVENTION: Vaccine and compositions for the TITLE OF INVENTION: prevention and treatment of Neisserial infections FILE REFERENCE: 875.0451831 FILE REFERENCE: 875.0451831 CURRENT APPLICATION NUMBER: US/10/066,551 PRIOR APPLICATION NUMBER: US 60/344,452 PRIOR APPLICATION NUMBER: US 60/344,452 PRIOR APPLICATION NUMBER: US 60/310,356	; PRIOR FILING DATE: 2003-07-15 ; PRIOR FILING DATE: 2002-01-31 ; PRIOR FILING DATE: 2001-01-31 ; PRIOR APPLICATION NUMBER: US 60/344,452 ; PRIOR FILING DATE: 2001-10-23 ; PRIOR PILING DATE: 2001-10-23 ; PRIOR FILING DATE: 2001-08-06 ; PRIOR FILING DATE: 2001-08-06 ; PRIOR FILING DATE: 2001-08-06 ; PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06 PRIOR FILING DATE: 2001-08-06 PRIOR FILING DATE: 2001-01-31 NUMBER OF SEQ ID NOS: 12 SEQ ID NO 4 LEIDTH: 525 TYPE: PRI	ο (
Neisseria gonorrhoea 4 97.2%;	Query Match 97.2%; Score 2643; DB 5; Length 525; Best Local Similarity 97.3%; Pred. No. 2.6e-226; Matches 511; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
Best Local Similarity 97.3%; Pred. No. 2.6e-226; Matches 511; Conservative 5; Mismatches 9; Indels 0; Gaps 0;  1 MHTDPKIQAMESETISPMKTRSLISLICLILICSCSWLPPIERTESRHFNTSKPVLLDN 60	1 MHTDPKIOAMPSETISPMKTRSLISLLCLLCSCSSWLPPLEBRTESRHFUTSKPVLLDN 60
1 MRANPKTQAMPSETISLMKTRSLISLCLLCSCSWLPPLEERTESRHFNTSKPVRLDN 60 61 ILQIRHTPHNNGLSDIYLLDDPHEALAARAALIESRHSLDLQYYIWRNDISGRLLFNLM 120	61 ILQIRHTPHNGLSDIYLLDDPHEALAARAALIESAEHSLDLOYYIWRNDISGRLLFNLM 
	CY 121 XLAAEKGVKKLLLDDNNTRGLDDLLGALDSHFNIEVRLFNPFVLRKKRALGYLTDFPKL 180
181 NRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWA 240	Db 181 NRRHINKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWA 240  Qy 241 SHSAHNATRIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWGSV 300  Db 241 SHSAHNATRIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWGSV 300
	301 QTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQD 
301 ÓTRLISÓDPAKGLÓRÐRRKPPÍAGRLÓÐALKÓPEKSVYLVSÞÝFVÞTKSGTÐALAKLVÓÐ 360	Qy 361 GIDVTVLTNSLQATDVAAVHSGYVKXRRPLLKAGIKLYELQPNHAVPATKDKGLTGSSVT 420

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----LLDDPHEALAARAALIESAEHSLDLQYYIWRN 109
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                                                                                                                                                                                                                                                                          APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.2%; Score 632; DB 4; Length 502; 32.8%; Pred. No. 4e-47; ive 93; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL
                                                                                                       481 TLDRHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIESLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...502
SEQUENCE DESCRIPTION: SEQ ID NO: 9085:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0 SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/993,002
RILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READBLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                     Sequence 9085, Application US/10335977; Publication No. US20040052799A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
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Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                 RESULT 7
US-10-335-977-9085
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Publication No. US2004025322A1

GENERAL INFORMATION

APPLICANT: Advectla, Michael A.

APPLICANT: Edwards, Jennifer L.

TITLE OF INVENTION: Vaccine and compositions for the prevention and treatment of Neis

TITLE OF INVENTION: Ancient and compositions for the prevention and treatment of Neis

TITLE OF INVENTION: Ancient and compositions for the prevention and treatment of Neis

TITLE OF INVENTION: Vaccine and compositions for the prevention and treatment of Neis

CURRENT APPLICATION NUMBER: US 10/621,184

PRIOR FILING DATE: 2003-09-19

PRIOR FILING DATE: 2003-09-19

PRIOR FILING DATE: 2003-09-13

PRIOR FILING DATE: 2001-01-31

PRIOR FILING DATE: 2001-01-31

PRIOR FILING DATE: 2001-01-31

PRIOR FILING DATE: 2001-01-31

NUMBER OF SEQ ID NOS: 32

LENGTHARE SESERE (or Windows Version 4.0)

LENGTH: 525
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GIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVT 420
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                                                                            421 SLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRV
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Pred. No. 2.6e-226;
5; Mismatches 9;
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Best Local Similarity
Matches 511; Conserv
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Sequence 356, Application US/09881752A

Sequence 356, Application US/09881752A

Patent No. US20020115078A1

GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Ownen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020115078A1e1 Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/041002
CURRENT APPLICATION NUMBER: US/09/881,752A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/813,457

PRIOR APPLICATION NUMBER: US 08/813,457
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                                                                                                                                                                                                                                                                                                                                                                                                                           205 FFGGVASKAKESFENYWRFHRSIPVS-LLRTHKRLKNNVKEIAKLHEKIPISAEDANEFE 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 LRYRETVEQSPLYQ-KIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQP 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 KDSVFIASSYFIPGKKIMKIFKNQISKGIELNILTNSLSSTDAIVVYGAWERYRNKLVRM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 GIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPATRKTY----PNEPEAKLWK 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |: ::| |::: :| |: :: :| :| :| :| 432 VLFDNPSFAKRVRLSLKDHA-QQSWHLVLYRH-RVIWE--ATEEGILIHEKNSPDTSFFL 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKA 393
                                                                                                                                                                                                  89
                                                                                                                                                                                                                                                               RKWRALGY - - - LTDFPRLNRRWHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDIL
                                                                                                                                                             64 IRHTPHNNGLSDIY-------LLDDPHEALAARAALIESAEHSLDLQYYIWRN
                                                                                                                                                                                      110 DISGRILFNIMYLAAERGVRVRILLIDDNNTRGLD----DLILALDSHPNIEVRLFNPFVL
                                                                                                                                                                                                                                                                                                                                             146 RN-KGLRYFEMLADYERIKKRMHNKLFIVDNFAVIIGGRNIGDNYFDNDLDTNFLDLDAL
                                                                                                                        26;
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                                                                                 ; Score 632; DB 4; Length 50; Pred. No. 4e-47; 93; Mismatches 181; Indels
                                                                               DB 4;
  ) LOCATION 1...502
) SEQUENCE DESCRIPTION: SEQ ID NO: 9086:
US-10-335-977-9086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 370
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 356
LENGTH: 428
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ORGANISM: Helicobacter pylori
                                                                                                                    Matches 161; Conservative
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RLIKEWSKVLP 498
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US-09-881-752A-356
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Best Local {
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                                                                                                                                         264 KKVNDFIERFÇKYQYPIYYG-----NAIFLADLPAK-IDTPLYS-PIKIAFEKALKNA 314
                                                                                                                                                                                                                                                                                                    ---GNIGKGLQALGYNDETSRHAL 274
                                                                                                                LRYRETVEQSPLYQ-KIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQP 333
                                                                                                                                                                                              EKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKA 393
                                                                                                                                                                                                                    GIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMG 453
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                                                                                                                                                                                                                                                                                                                                                                            RN-KGLRYFEMLADYERIKKRAMNKLFIVDNFAVIIGGRNIGDNYFDNDLDTNFLDLDAL 204
                                                             Sequence 9086, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                      ATGSVVGEVSHDFDRYWASHSAHNATRIIRS---
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APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible OPERATING SYSTEM: Windows NT 4.0 SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: SECTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 502 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 9086 SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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APPLICANT: Ferro, Josus Aparecido APPLICANT: Ferro, Josus Aparecido APPLICANT: De Oliveiro, Julio Cezar Franco APPLICANT: De Oliveiro, Julio Cezar Franco APPLICANT: De Laia, Marcelo Luiz APPLICANT: Setubal Joao C.
APPLICANT: Setubal Joao C.
APPLICANT: Furlan, Iuiz Roberto
TITLE OF INVENTION: Isolated Xanthomonas nucleic acid molecules, proteins encoded the TITLE OF INVENTION: uses thereof FILE REFERENCE: FAPESP 205.1 US
CURRENT APPLICATION NUMBER: US/10/418,861B
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US 60/374,620
PRIOR FILING DATE: 2002-04-22
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 DISGRLLFNLMYLAAERGVRVRLLLLDDNNTRGLD----DLLLALDSHPNIEVRLFNPFVL 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKWRALGY---LIDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDIL 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 IESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDSH 152
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                                                                                                                                                                                                                                                                                          Length 224;
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                                                                                                                                                                                                                                                                                   / Match 13.2%; Score 359; DB 4; Local Similarity 42.0%; Pred. No. 2.5e-23; les 81; Conservative 33; Mismatches 53.
                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...224
SEQUENCE DESCRIPTION: SEQ ID NO: 9084:
                                                                                                                    ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Farah, Shaker Chuck
Quaggio, Ronaldo Bento
Reinach, Fernando de Castro
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bublication No. US20040010131A1
GENERAL INFORMATION:
APPLICANT: da Silva, Ana Claudia Rasera
                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 ATGSVVGEVSHDF 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 FFGGVATDVQQNF 224
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ORGANISM: Xanthomonas
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Best Local Similarity
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                                                                                                                                          FEATURE
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                                               96 AEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLD----DLLLALDS 151
                                                                                                                                             152 HPNIEVRLFNPFVLRKWRALGY---LTDFPRLNRRMHNKSFTADNRATILGGRNIGDEYF 208
                                                                                                                                                                         161 ---HKRLK-NNAKEIAKLHEKIPISAEDKNQFEKKVNDFIDRFQKYQYPIYYGNAIFLAD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                     308 TPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 SPKK-IDTPLYS-PIKIAFEKALKNAKDSVFIASSYFIPGKKMMKIFKNQISKGIELNIL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTF 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428 IVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNR 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 VFDDNLTLLGSFNIDPRSAYINTESAVLFDNPSFAKRV------RLSLKDHAQ 378
                                                                                                                                                                                                                                          209 KVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDE 268
                                                                                                                                                                                                                                                                                                                                        TSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRL---------ISD 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||| :|| |: :|| |: | |:|| :|| TNSLSSTDAIVVYGAWERYRNQLVRMGANVYEIRNDFFNRQIKGR---FSTKHSLHGKTI 331
                                                                                             57
                                                                           SQKSIDMQTYIYKNDLSSQVIAKELLNAANRGVKVRILLDDN---GLDSDFSDIML-LNF
  Gaps
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Sequence 9084, Application US/20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELLCOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                           117 DNDLDTNFLDLDALFFGGVASKAKESFERYWRFHRSIPVS-LLRT---
Indels
80; Mismatches 146;
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APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 9084:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCE CHARACTERISTICS:
LENGTH: 224 amino acids
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 10
145; Conservative
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Matches
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Qy         176 DFPRINRRHHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDIL 222           Db         216 ESFFFSKLPLINLRMYNRNHRKIVVIDGTIGYVGENVGDEYIGKSKKFGYWRDTHLR 273           Qy         223 ATGSVVGEVSHDFDRYWASHSAH-NATRIIRSGNIGKGLOALGYNDETSRHAL 274           Db         274 IKGDAVNALQIRFILDWNSQSTRDNLTYESRYFPDVDSGGTIGIQIASSGPDE	RESULT 13   US-09628523A	OY 156 EVRLENPEVLRKWRALGYLTDFPRLNRRHNKSFTADNRATILGGRNIGD 205  199 KMANFDHFKSLGGEVEAFFASKLPILNFRMNRRHHKIIVIDGQLGYVGGFNIGD 253  OY 206 EYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGK 258  Db 254 EYLGLGKLGYWRDTHLRYGDADALQLRFILDWNS-QAHRQFEYDVKYFPKKGPLG-311  OY 259 GLQALGYNDETSRHALLRYRETVEOSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDR 315  Db 312
OY 153 PNIEVRLENPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKV 210  Bb agvertamper and the process of the	Oy 511 IAAMILSLL 519 Db 478 -FARLLSPL 485 Db 478 -FARLLSPL 485 Db 478 -FARLLSPL 485  RESULF 12 US-10-724-972A-3854 Sequence 3844, Application US/10724972A FRESULF 12 Sequence 3854, Application US/10724972A FRESULF 12 SEQUENCE 3854, Application US/10724972A FRESULF 12 FRESULF 12 FRESULF 12 FRESULF 12 FRESULF 13 FRESULF 13 FRESULF 13 FRESULF 14 FRESULF 15 FRESULF	Query Match   10.7%; Score 291; DB 4; Length 495;

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96 AEHSLDLOYYIWRNDISGRLLFNLMYLAAERGVRVRLLLLDDNNTRGLDDLLLALDSHPNI 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 493;
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APPLICANT: HARRIS, Douglas
APPLICANT: HARRIS, Douglas
APPLICANT: MOTT, John
TITLE OF INVENTION: ANTHRICKOBIAL METHODS AND MATERIALS
FILE REFERENCE: 00774.US1 CN1
CURRENT APPLICATION NUMBER: US/10/429,094
CURRENT FILING DATE: 2003-05-02
FRIOR APPLICATION NUMBER: US 09/966,521
FRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 145
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.5%; Score 286.5; DB 4;
21.1%; Pred. No. 2.4e-16;
live 86; Mismatches 169;
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469 KESYANRPLSVKFKESLAKLVS 490
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US-09-828-523A-90
US-09-828-523A-90
, Sequence 90, Application US/09828523A
; Patent No. US20020168697A1
, GENERAL INFORMATION:
                                                                                      Sequence 18, Application US/10429094; Publication No. US20030180821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-429-094-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 21.1%
Matches 106; Conservative
                                                                                                                                                   APPLICANT: TOMICH, Che-Shen APPLICANT: QUINN, Cheryl
                                                                          -10-429-094-18
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  376 VAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIF 435
                        436 IGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPAT 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 493;
                                                                                                                                                                                                                                                                              Sequence 18, Application US/09966521

Publication No. US20030087321A1

GENERAL INFORMATION:

APPLICANT: TOMICH, Che-Shen

APPLICANT: QUINN, Cheryl

APPLICANT: ARVIDSON, Staffan

APPLICANT: ARVIDSON, Staffan

APPLICANT: MOTT, John

TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS

FILE REFERENCE: 6212.N2

CURRENT APPLICATION NUMBER: US/09/966,521

CURRENT APPLICATION NUMBER: 2001-09-28

NUMBER OF SEQ ID NOS: 145

SOFFWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5%; Score 286.5; DB 3; 21.1%; Pred. No. 2.4e-16; ive 86; Mismatches 169;
                                                                                                  KESYANRPLSVKFKESLAKLVS 490
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LENGTH: 493
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Best Local Si
Matches 106,
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OTHER INFORMATION: Amino acid sequence encoded by S. aureus coding region cloned fc OTHER INFORMATION: expression in E. col
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                                                                                                                                                                                                                                 10.5%; Score 286.5; DB 3; Length 502; 21.1%; Pred. No. 2.5e-16; Live 86; Mismatches 169; Indels 141;
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TITLE OF INVENTION: ANTHRICROBIAL METHODS AND MATERIALS
FILE REPERENCE: 00774.051 CN1
CURRENT APPLICATION NUMBER: US/10/429,094
CURRENT FILING DATE: 2003-05-02
PRIOR PILITAGION NUMBER: US 09/966,521
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 145
SSCPUARR: PACENTIN Version 3.0
SEQ ID NO 84
LENGTH: 502
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      NUMBER OF SEQ ID NOS: 145
SOFTWARE: PatentIn version 3.0
SEQ ID NO 84
                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TOMICH, Che-Shen
APPLICANT: QUINN, Cheryl
APPLICANT: ARVIDSON, Staffan
APPLICANT: HARRIS, Douglas
APPLICANT: MOTT, John
                                                                                                                                                                                                                               Query Match
Best Local Similarity 21.19
Matches 106; Conservative
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US-10-429-094-84
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                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Amino acid sequence encoded by S. aureus coding region cloned for
; OTHER INFORMATION: expression in E. coli.
US-09-828-523A-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 AEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDSHPNI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVRLFNPFVLRKWRALG-----YLTDFP----RLNRRMHNKSFTADNRATILGGRNIGD 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 GLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQ---TRLISDTPAKGLDR 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRII------RSGNIGK 258
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                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score 286.5; DB 3; Length 502; 21.1%; Pred. No. 2.5e-16; Live 86; Mismatches 169; Indels 141;
APPLICANT: The Pharmacia & Upjohn Company
TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
FILE REFERENCE: 268.62120101
CURRENT APPLICATION NUMBER: US/09/828,523A
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/266,327
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: TOMICH, Che-Shen
APPLICANT: QUINN, Cheryl
APPLICANT: ARVIDSON, Staffan
APPLICANT: ARXIDSON, Staffan
APPLICANT: MOTT, John
TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
FILE REPERENCE: 6112.N2
CURRENT APPLICATION NUMBER: US/09/966,521
CURRENT FILING DATE: 2001-09-28
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Publication No. US20030087321A1
GENERAL INFORMATION:
                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 21.1%;
Matches 106; Conservative
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APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
APPLICANT: Bush, David
TITLE OF INVENTION: WUCLEIC ACID AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: PATH03-16
CURRENT APPLICATION WUMBER: US/10/724,972A
CURRENT FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR APPLICATION NUMBER: 09/134,001
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 PIAGRIQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 SGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.1%; Score 274.5; DB 4; Length 206; Best Local Similarity 31.4%; Pred. No. 7.6e-16; Matches 64; Conservative 45; Mismatches 84; Indels 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...206
SEQUENCE DESCRIPTION: SEQ ID NO: 9083:
                  ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---PNEPEAKLWKRIAAKILSLLP 520
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                                                                                                                                                                                        TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9083:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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SEQ ID NO 4379
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                                              encoded by S. aureus coding region cloned for
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                                                                                                                                                                                                                                                 42 EERTESRHFNTSKPVLLD-----NILQIRHTPHNNGLSDIYLLDDPHEALAARAALIES 95
                                                                                                                                            Query Match 10.5%; Score 286.5; DB 4; Length 502; Best Local Similarity 21.1%; Pred. No. 2.5e-16; Matches 106; Conservative 86; Mismatches 169; Indels 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DELICATION NO. CLEAR SMITH et al APPLICANTION:
APPLICANT: DOUGLAS SMITH et al APPLICANT: DOUGLAS SMITH et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                    FEATURE:
COTHER INFORMATION: Amino acid sequence
COTHER INFORMATION: expression in E. col-US-10-429-094-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTATIONS
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      496 RKTYPNEPEAKLWKRIAAKILS 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470 KESYANRPLSVKFKESLAKLVS 491
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; Publication No. US20040052799A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
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ORGANISM: Artificial
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US-10-335-977-9083
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Sequence 2, Application US/09848726
Patent No. US20020102667A1
GENERAL INFORMATION:
FALE SEPTICANT: NAMPOCHTRI, Madhavan
TITLE OF INVENTION: NO. US20020102667A1e1 Nucleotide Sequences Coding for the cls Ge
TITLE OF INVENTION: NO. US20020102667A1e1 Nucleotide Sequences Coding for the cls Ge
TITLE OF INVENTION: NO. US20020102667A1e1
TITLE OF INVENTION: NO. US20020102667A1e1
CURRENT APPLICATION NUMBER: US/09/848,726
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 500
ILENGTH: 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 GVRVRLLLD-------DNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRAL 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 PDESLLEAVTSACYRGVTVELFVS--EQADQFAIDHAQSSYYQALLEAGVKIYQF-PKPD 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPATKDKGLTGSSVTSLHAKTFIVD-----GKRIF--IGSFNLDPRSARLNTEMGVVIES 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V--------LHTKYMIADPDDTTGNEALGVLGSSNLDIRSFGLNYEISLMIAK 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                  92
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                                                                                                                                                                                                                                                                                                                                                                   67 TPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 GYLTDFPRLNRRMHNKSFTADNRATILGGRN-IGDEY-----FKVGEDTVFADLDILATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 PIVSSMEMIFAGDWYVESN-------EALDIRDHAEAHGYIGNTQKDSATN
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                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                 9.3%; Score 252; DB 4; Length 422;
23.4%; Pred. No. 2.3e-13;
tive 58; Mismatches 179; Indels 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 GNLIHEL-NALTDRYRTVSFKLTLDKWNQRSW-----RRRY 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      459 PKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPATRKTY 499
                                                                                                   TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                   Similarity 23.4
18; Conservative
                678
             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                   Best Local Sımı
Matches 108;
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                                           SEQ ID NO 78
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                                           11;
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                                                                                                                                    306 SDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVT 365
                                                                                                                                                                                                                        DNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTD--FP-----RLNRRMH 185
                                                                                                                                                                                                                                                                                             234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 LMIPC--KPDHPFVYWATFSNAADLLDSGVNIYTYQNGF------IHSK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 TFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKH 485
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APPLICANT: Schoder, Hartwig
APPLICANT: Schoder, Hartwig
APPLICANT: Schoder, Hartwig
APPLICANT: Schoder, Grar
APPLICANT: Zelder, Oskar
APPLICANT: ABSCHDAUE, GERGER
TITLE OF INVENTION: UNVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
TITLE OF INVENTION: TRANSPORT
FILE REFERENCE: BGI-125CPCN
CURRENT APPLICATION NUMBER: US/10/627,476
CURRENT APPLICATION NUMBER: 09/602,787
PRIOR PELING DATE: 1099-06-25
PRIOR PELING DATE: 1999-06-25
PRIOR PELING DATE: 1999-06-25
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-09
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                                           Gaps
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   22.3%; Pred. No. 6.2e-14;
ive 70; Mismatches 178; Indels 103;
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FILING DATE: 1999-07-09
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Publication No. US20040030116A1
GENERAL INFORMATION:
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APPLICANT: Kroger, Burkhard
                                 101; Conservative
Best Local Similarity
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SVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSP 285
                                                                                                                                                           313 LVQLIPSG-------PGYTTEPNLR-----MFNSIVHHAKERLILCSPYFI 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 LTDFPRLNRRMHNKSFTADNRATILGGRNIGDEYFKVGED----TVFADLDILATGSVVG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 EVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQS--PLY 287
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---RRFRRPDLRNHRKMLIIDGHTAFMGSQNLIAPSYLQKKNIKLGRE--WKDLMVELTG 268
                                                                                        -----EALDIRDHAEAHGYIGNTQKDSATN
                                                                                                                                                                                                                                                   286 LYQXIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFV
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23.8%; Pred. No. 4.4e-11;
tive 55; Mismatches 170; Indels
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APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAFAKI, YOSHIYUKI
APPLICANT: HATORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-272697
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; Publication No. US20030119018A1
; GENERAL INFORMATION:
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                                                                                     269 PIVSSMEMIFAGDWYVESN-
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Best Local Similarity 23.8%
Matches 100; Conservative
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SEQ ID NO 8603
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                                                ---rrfrrpdlrnhrkmliidghtafmgsqnljapsylqkkniklgrb---wkdlmveltg 269
                                                                                                                                                                                                  LYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFV 345
                                                                                                                                                                                                                                   LVQLIPSG------PGYTTEPNLR-----MFNSIVHAAKERLILCSPYFI 351
                                                                                                                                                                                                                                                                                        PTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHA 405
                                                                                                                                                                                                                                                                                                                  V-------LHTKYMIADPDDTTGNEALGVLGSSNLDIRSFGLNYEISLMIAK 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 GVRVRLLLD--------DINTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRAL 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 GVKVRLLFDHVGSWKYPGYHRLKKELNRMGFAWYLM--------LPLOPWR-- 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYLTDFPRLNRRMHNKSFTADNRATILGGRN-IGDEY----FKVGEDTVFADLDILATG 225
                                                                                                                                                      269 PIVSSMEMIFAGDWYVESN------EALDIRDHAEAHGYIGNTQKDSATN 312
                                                                                                                                                                                                                                                                                                                                                                                VPATKDKGLTGSSVTSLHAKTFIVD----GKRIF--IGSFNLDPRSARLNTEMGVVIES 458
                       --- FKVGEDTVFADLDILATG
                                                                                                          SVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 TPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAER
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23.4%; Pred. No. 3e-13;
iive 58; Mismatches 179; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      459 PKIAEQMERTLADTTPEYAYRVTLDKHNRLQWHDPATRKTY 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-4-07
PRIOR APPLICATION NUMBER: JP 00/189162
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 6514
LENGTH: 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HAYSHI, MIKIRO
APPLICANT: OCHIAL, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TEEDA, MASATO
APPLICANT: TEEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6514, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 23.4<sup>†</sup>
Matches 108; Conservative
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US-09-738-626-6514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 P----NIEVRLFNPFVLRKWRALGYLTDFPRL----NRRMHNKSFTADNRATILGGRNIG 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PKPIF-RAQVGKKVYQSL--- 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 VIVLINSLOATDVAAVHSGYVKYRK------PLLKAGIKLYELQPNHAVPATKDK 412
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               GENERAL INFORMATION:

APPLICANT: CHIRON SPA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
TITLE OF INVENTION: STREPTCCCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026926WO
CURRENT APPLICATION NUMBER: US/10/472,928
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
NUMBER OF SEQ ID NOS: 4979
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 212
LENGHAPE: 510
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Publication No. US20050136404A1
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 DEYINHVERFGYWKDSGIR-LDGLAVKALTRLFLTTWYINRGEIS-DFDGY-----HLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 IESAEHSLDLOYYIWRNDISGRLLFNLMYLAAERGVRVRLLLLDDNNTRGLDDLLLALDSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 LKKAEKFIFLEYYIIEEGLMWNRILDILEQKVAQGVEVKMLYDD---IGCMATLTGDYAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 RLRQLGİEAHKFNKVI-------PRLTVAYNNRDHRKILIVDGQIAYTGGVNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: cardiolipin synthetase (cls)
OTHER INFORMATION: Cellular location: membrane
OTHER INFORMATION: Similar to strain R6 sequence 15902224 (0.E+01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FADSQEVYPHSI-----KTSWYQ-------KLVKEIAQLFAPIL 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1%; Score 219; DB 5; Length 510;
21.4%; Pred. No. 2.7e-10;
ive 61; Mismatches 139; Indels 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 LADTTPEYAYRVTLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLL
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 NHSIPSDGLTIPYGSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
US20050020813A1
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Matches 101; Conservative 6
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US-10-617-320-3177
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US-10-472-928-212
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TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REFERENCE: AM100649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
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                                                                                                                                     466
                                                                                                                                                                       347 TKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAV 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 LISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGID 363
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                                                                                                                                  PATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQME
                                                                      DSYFVDLLCATARRGVQVQILLPG-PYTDQRACRLAGQHYYGTLLDAGVEIRQYQP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 510;
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8.1%; Score 219; DB 4; Le
Best Local Similarity 21.4%; Pred. No. 2.7e-10;
Matches 101; Conservative 61; Mismatches 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 225, Application US/10474776 Publication No. US20040110181A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 26
US-10-472-928-212
; Sequence 212, Application US/10472928
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SEQ ID NO 225
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7.5%; Score 205; DB 5; 1 llarity 21.1%; Pred. No. 2.8e-09; Conservative 64; Mismatches 151;
       RESULT 29
US-10-501-282-2186
US-quence 2386, Application US/10501282
; Publication No. US20050203280A1
                                                                                                     ; Sequence 2384, Application US/10501282; Publication No. US20050203280A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Alloiococcus otitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| :| :| :| || || :| DEYINHVERFGYWKDSGIR-LDGLAVKALTRLFLTTWYINRGEIS-DFDQY-----HLE 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 VTVLTNSLQATDVAAVHSGYVKYRK------PLLKAGIKLYELQPNHAVPATKDK 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 TRIIRSGNI----GKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTR 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 IESAEHSLDLOYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLLALDSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 VRIIT------PYIPDKKFIQLVTRGAYPDFLSAGVRIYEYSPGF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVI-ESP---KIAEQMERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.9%; Score 215; DB 5; Length 518; Best Local Similarity 21.2%; Pred. No. 6.2e-10; Matches 100; Conservative 61; Mismatches 140; Indels 170;
                                                                                                                                                                                                    FALON AFFLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptococcus pneumoniae
                                                                                     COMPUTER: CURNOWS
OPERATING SYSTEM: CUNKNOWN>
SOFTWARE: CUNKNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,320
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: misc_feature
) LOCATION: (B) LÖCATION 1...518
) SEQUENCE DESCRIPTION: SEQ ID NO: 3177:
US-10-617-320-3177
                                                                                                                                                                                                                                                                                                                              NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REPERENCE/DOCKET NUMBER: GTC-011
TELECOMUNICATION:
TELEPHONE: (781)893-5007
                                                                           MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 518 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3177: SEQUENCE CHARACTERISTICS:
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
                                                         COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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APPLICANT: RUSSELL, DOIN PARRISH
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: RUSSELL, DAVID PARRISH
TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
TILE REFERENCE: AN107080 L2
CURRENT APPLICATION NUMBER: 60/333,777
FRIOR PELING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: 60/323,777
PRIOR APPLICATION NUMBER: FCT/US02/36123
PRIOR FILING DATE: 2002-11-18
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: PCT/US02/36123
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 6653
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 2384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ILRIDENFVSYLNEKGIKTSVFNPL---DWR----LTF--QYNYRDHRKIMVVDGKIGYT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGRNIGDEYF----KVGE------------------DTVFADLDILATGSVVGEVSHDF--- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 GGMNIGDNYINRVEKAGHWKDGGIRLEGQGVWGFTTMF----LSLWDYLNDDTQDFRDF 167
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|| | || :|
-KLVKEIAQLFAPIL
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APPLICANT: MCMICHAEL, JOHN CALHOUN
APPLICANT: MCMICHAEL, JOHN CALHOUN
APPLICANT: ZAGURSKY, ROBERT JOHN
APPLICANT: ZAGURSKY, ROBERT JOHN
APPLICANT: ZAGURSKY, BAND BARRISH
APPLICANT: FLETCHER, LEAH DIANE
TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, INMUNOGENIC COMPOSITIONS AND USES THEREOF
FILE REFERENCE: AMIOO780 L2
CURRENT APPLICATION NUMBER: US/10/501,282
CURRENT APPLICATION NUMBER: 60/426,742
PRIOR APPLICATION NUMBER: 60/426,742
PRIOR APPLICATION NUMBER: E07/US02/36123
PRIOR FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: PCT/US02/36123
PRIOR FILING DATE: 2002-11-25
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CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: 60/333,777
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: PCT/US02/36123
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 6653
SOFTWARE: PatentIn version 3.2
LENGTH: 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Alloiococcus otitidis
US-10-501-282-2388
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Best Local S
Matches 92
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                                      APPLICANT: MCMICHAEL, JOHN CALHOUN
APPLICANT: ZAGURSKY, ROBERT JOHN
APPLICANT: ZAGURSKY, ROBERT JOHN
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: FLETCHER, LEAH DIANE
TITLE OF INVENTION: ALLOICOCCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
FILE REFERENCE: AM100790 L2
CURRENT APPLICATION NUMBER: US/10/501,282
CURRENT PILING DATE: 2004-07-09
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Publication No. US20050203280A1
GENERAL INFORMATION:
APPLICANT: MCMICHAEL, JOHN CALHOUN
APPLICANT: ZAGURSKY, ROBERT JOHN
APPLICANT: RUSSELL, DAVID PARRISH
APPLICANT: RISSELL, DAVID PARRISH
APPLICANT: RISTELCHER, LEAH DIANE
TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES TFILE REFERENCE: AM100780 L2
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                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/33,777
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: 60/426,742
PRIOR FILING DATE: 2002-11-18
PRIOR PLING DATE: 2002-11-25
PRIOR PLING DATE: 2002-11-25
NUMBER OF SEC ID NOS: 6653
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Alloiococcus otitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 LADTTPEYAYRVTLDKH 485
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US-10-501-282-2388
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LOCATION: (226)...(246)
OTHER INFORMATION: Phospholipase D Active site proteins motifs. domain
OTHER INFORMATION: identified by eMATRIX, accession number PF00614B, p-value=4.774e-
OTHER INFORMATION: 14, raw score of 14.45
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (108)...(248)
OTHER INFORMATION: Phospholipase D. Active site motif domain identified by OTHER INFORMATION: accession name PLDC, E-value=7e-10, PFam score of 46.3
                                                                                        80 DDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDD-NN 138
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Query Match 7.5%; Score 205; DB 5; Length 512; Best Local Similarity 21.1%; Pred. No. 4.7e-09; Matches 92; Conservative 64; Mismatches 151; Indels 130;
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; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790C1P3/US
; CURRENT APPLICATION NUMBER: US/10/450, 763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR PILING DATE: 2001-03-30
; PRIOR PILING DATE: 2000-03-31
; PRIOR PILING DATE: 2000-03-31
; PRIOR FILING DATE: 2000-08-23
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SOFTWARE: Custom
SEQ ID NO 31511
LENGTH: 280
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GENERAL INVENTATION:

APPLICANT: MCMICHAEL, JOHN CALHOUN

APPLICANT: ENGSELL, DAVID PARRISH

APPLICANT: RUSSELL, DAVID PARRISH

APPLICANT: RUSSELL, DAVID PARRISH

APPLICANT: RUSSELL, DAVID PARRISH

TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING

TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF

TITLE OF INVENTION: POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF

TITLE OF INVENTION NUMBER: 00/407-09

PRIOR APPLICATION NUMBER: 60/433,777

PRIOR APPLICATION NUMBER: 60/426,742

PRIOR PILING DATE: 2002-11-18

PRIOR FILING DATE: 2002-11-25

NUMBER OF SEQ ID NOS: 6653

SOFTWARE: PATCHIN VERSION 3.2

SEQ ID NO 2392

LENGTH: 512

LENGTH: 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 DDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDD-NN 138
                                                                                                                                                                                                                                                                                                       139 TRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATIL 198
                                                                                                                                                                                                                                                                                                                                                                                               -----DIVFADLDILATGSVVGEVSHDF--- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- DRYWASHSAHNATRIIRSGNIGKGLQALGY----NDETSRHALLRYRETVEQSPLYQ 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 KLYSALENAALSGVDVRIVTPGI--PDKKIVFETTQSFYDKLLEVGVKIYEYAPGF---- 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 GGMNIGDNYINRVEKAGHWKDGGIRLEGQGVWGFTTMF----LSLWDYLNDDTQDFRDF 297
                                                                                                                                                                                7.5%; Score 205; DB 5; Length 493;
21.1%; Pred. No. 4.5e-09;
tive 64; Mismatches 151; Indels 130;
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Publication No. US20050203280A1
GENERAL INFORMATION:
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                                                                                        ; TYPE: PRT
; ORGANISM: Alloiococcus otitidis
US-10-501-282-2390
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457 FDNLFP-ICRQVSLEEN 472
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; ORGANISM: Alloiococcus otitidis
US-10-501-282-2392
                       SOFTWARE: PatentIn version 3.2
SEQ ID NO 2390
                                                                                                                                                                                                                               92; Conservative
  NUMBER OF SEQ ID NOS: 6653
                                                                                                                                                                                                          Similarity
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US-10-501-282-2392
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Best Local S:
Matches 92,
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Query Match

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                                                                                                                                                                                                                                HNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRL 304
                                                                                                                                                                                                                                                                                                                                                                                         365 TVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHA 424
                                                                                                                                                                                                                                                                                                                                                                                                                96 AEHSLDLQYYI-----WRNDISGRLLFNLMYLAAERGVRVRLLLLDDNNTRGLDDL-LLA 148
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                  301 GYGSPDLSDEFVNELTAAGVVFRYYDP----RPRLFGMRTN---VFRRMHRKIVVIDARI
                                                                            DNNTRGLDDLLLALDSHPNI EVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zagursky, Robert
APPLICANT: Nickbarg, Elliot
APPLICANT: Nickbarg, Elliot
APPLICANT: Wincher, Lourie
TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
FILE REFERENCE: AM 100399
CURRENT APPLICATION NUMBER: US/10/474,792
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 674
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                        6.2%; Score 168.5; DB 5;
20.0%; Pred. No. 8.8e-06;
iive 63; Mismatches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 354, Application US/10474792; Publication No. US20040236072A1; GENERAL INFORMATION: APPLICANT: Olmsted, Stephen
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Best Local Similarity
Matches 89; Conserv
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US-10-474-792-354
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                                      12;
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                                                                                                                                               136 DNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRA 195
                                                                                                                                                                       GYGSPDLSDEFVNELTAAGVVFRYYDP----RPRLFGMRTN---VFRRMHRKIVVIDARI 123
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                                                                                                                                                                                                                            196 TILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFD------RYWASHSA 244
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                                                                                              76 IYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLD
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                                      Gaps
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                Pred. No. 8.9e-07;
1; Mismatches 122; Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------SGYY----LVKGGVQVFEYRR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 KVALMDDHWATVGSSNLDPLSLSLNLEANVIIHD----RHFNOTLRD 270
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GENERAL INVOCATION.

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790CTP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR PILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: Custom

SEQ ID NO 31510
                                                                                                                                                                                                                                                                                                                                               181 HKAEENROPGE----AQANGY-----AVVRF----
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. Sequence 31510, Application US/10450763

. Publication No. US20050196754A1

. GENERAL INFORMATION:
20.4%; Pic.
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Best Local Similarity 20.4%
Matches 83; Conservative
                                  83; Conservative
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              Best Local Similarity
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NAME/KEY: DOMAIN
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APPLICANT: Frohman, Michael
APPLICANT: Frohman, Michael
APPLICANT: Frohman, Morris, Andrew
APPLICANT: Engelbrecht, Joanne
APPLICANT: Engelbrecht, Joanne
APPLICANT: ENGENCE: Oxyx2004-D1V2
CURRENT APPLICATION NUMBER: US/10/137,129A
CURRENT APPLICATION NUMBER: 09/536,224
PRIOR APPLICATION NUMBER: 09/536,224
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 GRIDWQSVQTRLISDTP-----AKGLDRDRRKPPIAGRLQDA-----LK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LPKSTSTANNLPFMIPGGQCATVQVLRSVDRWS-----AGTLENSILNAYLHTIR 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VKYRKPLLKAGIKLYELQPNH 404
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  372 EKLKPYERV------SIYEFAIWETQLHKKCMIIDDEIFVIGSYNFGKKSDAFDY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 ----HPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIG---
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4.9%; Score 133.5; DB 4;
Best Local Similarity 18.6%; Pred. No. 0.028;
Matches 101; Conservative 80; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 QPEKSVYLVSPYFVPTKSGTDALAKLVQDGID-
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                                                                                                                                                                               Sequence 6, Application US/10137129A; Publication No. US20030124108A1; GENERAL INFORMATION:
                                           467
                                                                   421 ESIVVIESPEVAAKANK 437
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                                           EMGVVIESPKIAEOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-137-129A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 RIA 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 QTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSG 350
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                                                                                     KTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTL-- 482
                                                                                                                            ---YLYRVSVIA 483
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365 TVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHA 424
                                           -----VHS 444
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                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCRMAIL: CHIRON SPA

TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
FILE REFERENCE: PO25035W

CURRENT APPLICATION NUMBER: US/10/312,273

CURRENT APPLICATION NUMBER: US/10/312,273

CURRENT FILING DATE: 2002-12-20

PRIOR PLICATION NUMBER: 0017047.2

PRIOR FILING DATE: 2000-07-03

PRIOR PLICATION NUMBER: 0017047.2

PRIOR APPLICATION NUMBER: 0017043.8

PRIOR PLILING DATE: 2000-07-11

PRIOR PLILING DATE: 2000-00-21

PRIOR PLILING DATE: 2000-08-18

PRIOR FILING DATE: 2000-08-18

PRIOR FILING DATE: 2000-08-18

PRIOR FILING DATE: 2000-08-18

PRIOR FILING DATE: 2000-09-14

PRIOR FILING DATE: 2000-09-14

PRIOR FILING DATE: 2000-09-14

PRIOR FILING DATE: 2000-09-14

PRIOR FILING DATE: 2000-09-14

PRIOR FILING DATE: 2000-01-10

PRIOR FILING DATE: 2000-11-10

PRIOR FILING DATE: 2000-11-10

PRIOR FILING DATE: 2000-11-10

PRIOR FILING DATE: 2000-11-10

PRIOR FILING DATE: 2000-11-10

PRIOR FILING DATE: 2000-11-10

PRIOR FILING DATE: 2000-11-10

PRIOR SEQUING OF 550

NUMBER OF SEQ ID NOS: 664

SOFTWARE: SEGWING9, version 1.02
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                        DB 4;
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                                                                                                                      445 KVFISDNTKAVVGTINLDYRSLYHHFECAT-
                                                                                                                                                                    483 ------DKHNRLQWHDPATRKTY 499
                                                                                                                                                                                                           484 DIVNDFNEAOKOSLLMTSDHLTORPW 509
                                                                                                                                                                                                                                                                                                                ; Sequence 75, Application US/10312273; Publication No. US20040005667A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-75
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Best Local Similarity 22.89
Marches 86; Conservative
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US-10-312-273-75
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Publication No. US20050106162A1

GENERAL INFORMATION:

APPLICANT: Grandi, Guido

APPLICANT: Ratti, Giulio

TILE OF INVENTION: Immunisation Against Chlamydia Trachomatis

FILE REFERENCE: 002441.00085

CURRENT APPLICATION NUMBER: US/10/498,327

CURRENT FILING DATE: 2004-10-6-10

PRIOR APPLICATION NUMBER: PCT/IB02/05761

PRIOR FILING DATE: 2002-12-12

NUMBER OF SEQ ID NOS: 262

SOFTWARE: Patentin version 3.2

SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                       4.7%; Score 127; DB 5; Length 474;
20.3%; Pred. No. 0.038;
tive 89; Mismatches 194; Indels 102;
                                                                                                                                                                                                                                                                       ; ORGANISM: Chlamydia trachomatis
US-10-498-327-79
                                                                                                                                                                                                                                                                                                                                                       98; Conservative
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Best Local Similarity
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US-10-498-327-79
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Sequence 2203, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Pahy, Eoin D.
APPLICANT: Zhang, Bing
APPLICANT: Ghoson, Bradford W.
APPLICANT: Gibson, Steven W.

US-10-408-765A-2203

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Sequence 215690, Application US/10424599
; Sequence 215690, Application US/10424599
; Sequence 215690, Application No. US20040031072A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa Thomas J
    APPLICANT: Covalic David K
; APPLICANT: Cao Yongwei
    TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    FILE REFERENCE: 38-21(53223)B
    CURRENT APPLICATION NUMBER: US/10/424,599
    CURRENT FILING DATE: 2003-04-28
    NUMBER OF SEQ ID NOS: 285684
    SEQ ID NO 215690
    LENGTH: 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 VVGEVSHDFDRYWASHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 YQKIQTGRIDWQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDA-----LKQPEKSVY 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --TLPGGQC--TTVQV-----LRSVDRWS-----AGTLENSILNAYLHTIRESQHFLY 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 LQATDVAAVHSGY------VKYRKPLLKAGIKLYELQPNHAVPATKD 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 --------EYFKVGED-------TUFADLDILATGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 LVSPYFVPTKSGTDALAKLVQDGID------VTVLT------NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 EQMERTLADITPEYAYRVTLDKHNR--LQWHDPATRKTYPNEPEAKLWKRIA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ::::||:::|| EYQAGRFALSLRKHCFGVILGANTRPDLDLRDPICDDFF-----QLWQDMA 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6%; Score 124.5; DB 4; Length 548;
18.0%; Pred. No. 0.079;
tive 76; Mismatches 145; Indels 215;
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERENCE: 660088 445
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 LTDFPRLNRRMHNKSFTADNRATILGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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US-10-424-599-215690
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482
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                                                                                                                                                                 116 LFNLMYLAAERGVRVRLLLDDNNT-----RGL---DDLLLALDSHPNIEVRLFNPFV 164
                                                                                                                                                                                                                                165 LRKWRALGYLTDFPRLNRRMHNKSFTADNRA-----TILGGRNIGDEYFKVGEDT 214
                                                                                                                                                                                                                                                   -----DLDILATGSVVGEVSHDFDRYWASHS 243
                                                                                                                                                                                                                                                                                                                    : | :: |: | 135 LFQTLTEESHYHDFYQTNIAGASLNKGGPREPWHDAHASVTGDAAWDVLTNFEQRWTKQC 194
                                                                                                                                                                                                                                                                                                                                                                 244 AHNATRIIRSGNIGKGLQALGYNDETSRHALLRYR--ETVEQSPLYQKIQTGRIDWQSVQ 301
                                                                                                                                                                                                                                                                                                                                                                                       ---- 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 IIESGEPGHPRDYLNFFCLANREKKGKEEY-LSPHSPHPETQYWNAQKNRRFP----VYV 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
                                                                                                                                                                                  26 LGELLKKKAEEGVAVRVMIWDDETSLPFIKNKGVMKTHDEDAFAYFKHTKV-----1
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                                                                                            Query Match
4.5%; Score 122.5; DB 4; Length 553;
Best Local Similarity 18.2%; Pred. No. 0.12;
Matches 92; Conservative 79; Mismatches 167; Indels 167; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 302 TRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYF-----
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; CHER INFORMATION: Clone ID: PAT_MRT3847_36797C.1.pep
US-10-424-599-215690
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Search completed: May Job time: 170 secs

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61 ILQIRHTPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLM 120
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GENERAL INFURNALION.

APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PONTANA Maria Rita
APPLICANT: MASIGNAIN Vega
APPLICANT: MASIGNAIN Vega
APPLICANT: MORACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFREENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 5462

LENGTH ....
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ORGANISM: Neisseria gonorrhoeae
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Best Local Similarity
Matches 523; Conserv
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Sequence 2518, Ap
Sequence 2698, Ap
Sequence 1133, Ap
Sequence 1000, Ap
Sequence 1814, Ap
Sequence 238, App
Sequence 238, App
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2720
1 MHTDPKIQAMPSETISPMKT......KLWKRIAAKILSLLPIEGLL
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1: /SIDS5/ptodata/2/pubpaa/USG8_NEW_PUB.pepl:*
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12: /SIDS5/ptodata/2/pubpaa/USG1_NEW_PUB.pep:*
GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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11 US-11-045-004-2518

11 US-11-045-004-2698

11 US-11-079-463-7133

9 US-10-93-62-1000

11 US-11-079-463-7814

11 US-11-079-463-7814

11 US-11-074-176-10

9 US-10-510-386-30

11 US-11-098-666-10938

9 US-10-510-386-30

10 US-11-098-666-10938

9 US-10-42-586-42

9 US-10-243-136-42

9 US-10-243-136-42

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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Sequence 42, Appl Sequence 42, Appl Sequence 2, Appl Sequence 15, Appl Sequence 15, Appl Sequence 7533, App Sequence 27848, A Sequence 27846, A Sequence 85, Appl Sequence 85, Appl Sequence 85, Appl Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30809, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 30808, A Sequence 308
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Sequence 9468, Ap
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Sequence 179, App
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                             US-10-243-345-42

US-10-243-357-42

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US-10-247-013-42

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US-11-026-701-15

US-11-096-568A-27848

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TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
SHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSV
                                                             QTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPBKSVYLVSPYFVPTKSGTDALAKLVQD
                                                                                                   GIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVT
                                                                                                                                                    SLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEOMERTLADTTPEYAYRV
                                                                                                                                                                                                                  TLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525
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CHARBIT, ALAIN
URANT, LIONEL
PEREZ-DIAZ, JOSE-CLAUDIO
BAQUERO, FERNANDO
GARCIA DEL PORTILLO, FRANCISCO
GOMEZ-LOPEZ, NURIA
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CURRENT APPLICATION NUMBER: US/11/045,004
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: 10/637,657
PRIOR FILING DATE: 2003-08-11
                                                                                                                                                                                                                                                                                         Sequence 2218, Application US/11045004
Publication No. US20060078901A1
GENERAL INFORMATION:
APPLICANT: BUCHRIESER, CARMEN
APPLICANT: FRANGEUL, LIONEL
APPLICANT: COUVE, ELISABETH
APPLICANT: FSIHI, HAFIDA
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DOMINGUEZ-BERNAL, GUSTAVO
GARRIDO-GARCIA, PATRICIA
TIERREZ-MARTINEZ, ALBERTO
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CHAKRABORTY, TRINAD
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ENTIAN, KARL-DIETER
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CHETOUANI, FARID
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KUHN, MICHAEL
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WEHLAND, JURGEN
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ROSE, MATTHIAS
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HAIN, THORSTEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                            19 KTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDNILQIRHTPHNNGLSDIYL
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                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                   10.8%; Score 294.5; DB 11; Length 504; 23.5%; Pred. No. 4.1e-16; tive 72; Mismatches 207; Indels 109;
PRIOR FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: PCT/FR01/01118
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 2684
SOFTWARE: PREENTIN version 3.3
LENGTH: 504
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                                                                                                                                                                                                                                       ; ORGANISM: Listeria monocytogenes
US-11-045-004-2518
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DEHOUX, PIERRE
DUSSURGET, OLIVIER
CHETOUANI, FARID
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APPLICANT: FRANGEUL, LIONEL
APPLICANT: COUVE, ELISABETH
APPLICANT: RUSNIOK, CHRISTOPHE
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GLASER, PHILIPPE
KUNST, FRANCK
COSSART, PASCALE
DANIELS, JUSTIN
GOEBEI, WERNER
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Best Local Similarity 23.54
Matches 119; Conservative
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APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
TITLE OF INVENTION: NUCLEIC AND THERAPEUTICS
FILE REPERBNCE: PATHO0-03DIV2
CURRENT FILLING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR APPLICATION NUMBER: US 60/128,705
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 7133
  476
                         184 MHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDF--DRYWAS 241
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Publication No. US2005025478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TILLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
425 KTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLAD-----TTPE-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 PHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 VRVRLLLDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFP----RLNRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 8.9%; Score 241.5; DB 11; Length Best Local Similarity 23.2%; Pred. No. 9.4e-12; Matches 94; Conservative 60; Mismatches 163; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 TSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQM
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                                                                                                                                                                                                                                             Sequence 7133, Application US/11079463
Publication No. US20060073161A1
GENERAL INFORMATION:
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US-11-079-463-7133
                                                                                    477 AYR 479
                                                                                                                                 462 AKR 464
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 SDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLL 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 YDAMGSRITKKSFFRIFQKNGGLVRPFPSKLP----LINF-RLNYRNHRKLAIIDG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 RATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRS 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 GKAVYAMQTRFIMDWNSASSTHKIDYKARYFPTFHGKGHTSMQIVSSGPDSEWQQIKNGY 322
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---MINAAKKTIYLQSPYFIPDASLLEAIKIAALSGVDV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/11/045,004
CURRENT FILING DATE: 2005-01-28
PRIOR PILLING DATE: 2003-08-11
PRIOR FILING DATE: 2003-08-11
PRIOR PILLING DATE: 2002-10-08
PRIOR PILLING DATE: 2001-04
PRIOR APPLICATION NUMBER: PCT/FR01/01118
PRIOR APPLICATION NUMBER: PCT/FR01/01118
PRIOR PILLING DATE: 2001-04-11
PRIOR PILLING DATE: 2000-04-11
NUMBER: OF SEQ ID NOS: 2854
                                                                                                                                                                                                                                                                                PEREZ-DIAZ, JOSE-CLAUDIO
BAQUERO, FERNANDO
GARCIA DEL PORTILLO, FRANCISCO
                                                      DOMINGUEZ-BERNAL, GUSTAVO
GARRIDO-GARCIA, PATRICIA
TIERREZ-MARTINEZ, ALBERTO
                                   VAZQUEZ-BOLAND, ANTONIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT / ORGANISM: Listeria monocytogenes US-11-045-004-2698
                                                                                                                                                                                                                                                                                                                                                     GOMEZ-LOPEZ, NURIA
MADUENIO, ENCARNA
PABLOS, BETRIZ DE
WEHLAND, UURGEN
KARST, UWE
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                                                                                                                            AMEND, ALEXANDRA CHAKRABORTY, TRINAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                         HAIN, THORSTEN
BERCHE, PATRICK
CHARBIT, ALAIN
DURANT, LIONEL
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Best Local Similarity 25.5%
Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        170 KIAVIDGKIGYTGGMNIADYYINGLPKIG---TWRDMHIRIEGDAVNILQEIFLDIWNKT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 SAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQT 302
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                                                                                                                                                           18 SIGTARTONIDSLLM------OREDTICFIRSDSLVL-OFLEYSNIPITDN-
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; Bedication No. US20050250135A1
; CENERAL INFORMATION:
; APPLICANT: Riaenhamer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric.
; APPLICANT: Altermann, Eric.
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-64
; CURRENT FILING DATE: 2005-03-07
; DIOL AND AND APPLICATION NUMBER: US/11/074,176
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                                                                     70; Mismatches 196; Indels 109;
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                          DB 11; Length 429;
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Pred. No. 1.3e-10;
65; Mismatches 172;
                          Score 229.5; DB 1
Pred. No. 7.2e-11;
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PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
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US-11-074-176-10
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Best Local Similarity 22.7%
Matches 99; Conservative
                          Query Match
Best Local Similarity 21.9%
Matches 105; Conservative
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Sequence 7814, Application US/11079463
Publication No. US2006073161A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/11/079,463
CURRENT PILING DATE: 2005-03-14
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1099-04-09
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 7814
LENGTH: 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 NATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLI 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      316 SSGPAFDLHQ-----IEYGYTKMIMSAKKSIYLQSPYFIPDQSYINALKWAANSGVEVN 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 IDLFTDGHKLYEKVLEDIYNAQDYIHLEYYTFELDGLGKRILDALETKLKEGLEVKLLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88;
                                                                                                                                                                                                                                                                                                                                                                                                                                           8.5%; Score 232; DB 9; Length 442; 22.8%; Pred. No. 4.7e-11; tive 57; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LMIPC--KPDHPFVYWATFSNAADLLDSGVNIYTYQNGF--
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CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                       NAME/KEY: MOD RES
LOCATION: (442)
OTHER INFORMATION: variable amino acid
                                                                                                                                                         LENGTH: 442
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 22.8
Matches 89; Conservative
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ORGANISM: B.fragilis
US-11-079-463-7814
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22.4%; Pred. No. 1.1e-10;
tive 58; Mismatches 177;
                                                               276 УLVР--МКРЫНРLVКЕААҮТНГРАLLKAGCYIYRYY-
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APPLICANT: Clausen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Olsen, Steen Troels
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OP INVENTION: Improved Bacillus Host Celler REFERENCE: 10294.204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 30, Application US/10510386; Publication No. US20050244922A1; GENERAL INFORMATION:
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APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Orgensen, Steen Troels
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REPERENCE: 10294.204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: Patentin version 3.3
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Publication No. US20050244922A1
GENERAL INFORMATION:
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US-10-510-386-238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PKLSINLR 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 SAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQT 302
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                                                         APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-12801
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT APPLICATION NUMBER: DCT/US03/31318
PRIOR PILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEC ID NOS: 11433
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH. A70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Biosynexus Incorporated
APPLICANT: Boster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629W0
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
Sequence 10838, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 127, Application US/10485517
Publication No. US20050256299A1
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US-10-485-517-127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 NIGKGLQALGYNDETSRHALLRYRE----TVEQSPL-----YQKIQTGRIDW----- 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       821 AKYADRIFYVIKERAHGNETYVLL------SH-NIP 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---KVGEDT-VFADL-----DILATGSVVGEVSHDFDRYWASHSAHNATRIIRSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 DALAKLVQDGIDVT---VLTNS-----LQATDVAAVHSGYVKYRK------
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APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
APPLICANT: MASIGNAIN Vega
APPLICANT: MASIGNAIN Vega
APPLICANT: MASIGNAIN Vega
TITLE OF INVERTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SEQ ID NOS: 9218
SEQ ID NO 4224
SEQ ID NO 4224
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                                                                                                                                                                                                                                                                                                  4.0%; Score 108.5; DB 9;
19.8%; Pred. No. 3.4;
atrive 64; Mismatches 143;
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                                                                                                                                                                                                                   ORGANISM: Staphylococcus aureus US-10-485-517-127
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: Patentin version 3.1
LENGTH: 1263
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Best Local Similarity
Matches 101; Conserv
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284 SPLYQKIQT-GRIDWQSVQTRLISDTPAKGLDRDRRKP----PIAGRLQDALKQPEKSVYL 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 VSPYFVPT-----KSGTDALAKLVQ---DGIDVTVLTNS----LQATD--VAAV 379
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          PRIOR APPLICATION NUMBER: 10/19742

PRIOR APPLICATION NUMBER: 10/19742

PRIOR PLING DATE: 1997-09-17

PRIOR PLING DATE: 1997-10-9-17

PRIOR PLING DATE: 1997-10-24

PRIOR FLING DATE: 1997-11-20

PRIOR FLING DATE: 1997-11-10-24

PRIOR FLING DATE: 1997-11-10

PRIOR PLING DATE: 1997-11-10

PRIOR PLING DATE: 1997-11-10

PRIOR PLING DATE: 1998-03-27

PRIOR PLING DATE: 1998-05-22

PRIOR PLING DATE: 1998-06-18

PRIOR PLING DATE: 1998-06-18

PRIOR PLING DATE: 1998-06-24

PRIOR PLING DATE: 1998-06-18

PRIOR PLING DATE: 1998-06-18

PRIOR PLING DATE: 1998-06-24

PRIOR PLING DATE: 1998-06-24

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PRIOR PLING DATE: 1998-06-18

PRIOR PLING DATE: 1998-06-24

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P943-0016154
CURRENT APPLICATION NUMBER: US/10/242,902
CURRENT FILING DATE: 2002-09-13
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Best Local Similarity 25.0%; Pred. No. -
Marches 53; Conservative 33; Mismatches
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
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Publication No. US20060073549A1
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Watanbe, Colin
Wood, William
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baker, Kevin
APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, E
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                               103 VPVATAMOKLPPV-----PFLAGRTFWLKTGQTLDIGRLKTDLVDAGYNHVSHVVAAGE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 ATILGGRNIGDEYFKVGEDTVFA-------DLDILLATGSVVGEV----SHDFD 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 -----TDSEAOKIFRS----------RFREEVDGNPNDAAVYKAVSN 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 ----ALDSHPNIEVRLFNPFVLRK--WRALGYLTDFPRLNRRM-----HNKSFTADNR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----WQSVQTRLISDTPAK 311
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APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C21
CURRENT APPLICATION NUMBER: US/10/242, 586
                                                                                                                      Indels 235; Gaps
                                                                    Query Match
3.9%; Score 105.5; DB 9;
Best Local Similarity 20.7%; Pred. No. 5.7;
Matches 127; Conservative 63; Mismatches 190;
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Filvarceff, Ellen
Goddard, Audrey,
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 GLDRDRRKPPI------
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ell
APPLICANT: Goddard, Audre
APPLICANT: Grimald, J.
APPLICANT: Grimald, J.
APPLICANT: Smith, Victori
APPLICANT: Stephan, Jean
APPLICANT: Stephan, Jean
APPLICANT: Watanbe, Colin
APPLICANT: Wood, William
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Length 489;

DB 9;

71; Indels

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APPLICANT: Baker, Kevin
APPLICANT: Baton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Smith, Victoria
APPLICANT: Smeth, Victoria
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
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PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/05114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 42, Application US/10243136; Publication No. US20060074228A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Conservative
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CORGANISM: Homo Sapien
US-10-243-116-42
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LENGTH: 489
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Matches 5
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APPLICANT: Zhang, Zherman

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE PS 303 (15.88)

CURRENT APPLICATION NUMBER: US/10/243,116

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: 10/197942

PRIOR APPLICATION NUMBER: 60/059114
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 42
LENGTH: 489
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PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08901
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090657
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
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Sequence 42, Application US/10243116

Publication No. US20060073550A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Baton,Dan

APPLICANT: Filoaroff, Ellen

APPLICANT: Goddard, Audrey

APPLICANT: Grimalid, J. Christopher

APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Stephan, Jean-Phillippe

APPLICANT: Watanbe, Colin

APPLICANT: Matanbe, Colin

APPLICANT: APPLICANT: Anny Zemin
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ORGANISM: Homo Sapien
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284 SPLYQKIQT-GRIDWQSVQTRLISDTPAKGLDRDRRKP---PIAGRLQDALKQPEKSVYL 339
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PRIOR APPLICATION UNMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR PELICATION NUMBER: 60/065027
PRIOR PELICATION NUMBER: 60/065027
PRIOR PELICATION NUMBER: 60/079689
PRIOR PILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR PILING DATE: 1998-05-22
PRIOR PILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PELICATION NUMBER: 60/080801
PRIOR APPLICATION NUMBER: 60/080689
PRIOR PILING DATE: 1998-06-28
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
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TIPLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENERNCE: 95630R1032
CURRENT APPLICATION NUMBER: US/10/243,136
CURRENT FILING DATE: 2002-09-12
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APPLICANI: WOOL, WILLIAM
APPLICANI: Zhang, Zemin
APPLICANI: Shang, Zemin
APPLICANI: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: 93630R.C27
CURRENT APPLICATION NUMBER: 10/197942
PRIOR PILING DATE: 2002-09-12
PRIOR PLLING DATE: 1970-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR PLLING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 VSPYFVPT-----KSGTDALAKLVQ---DGIDVTVLTNS----LQATD--VAAV 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 ASYYWSLTGPDIGVNDSSSQLGEALLQKLQQLLGRNISLAVATSSPTLARTSTDLQVLAA 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55; Gaps
                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.8%; Score 104.5; DB 9; Length 4
25.0%; Pred. No. 1.7;
tive 33; Mismatches 71; Indels
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PRIOR PILING DATE: 1988-03-27
PRIOR PELLING DATE: 1988-03-27
PRIOR PELLING DATE: 1988-03-27
PRIOR PELLING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wod, William
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Publication No. US20060073551A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin
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LENGTH: 489
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Matches 5
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APPLICANT: Goddard, Audren
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Suith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Prong, Sherman
APPLICANT: Prong, Sherman
APPLICANT: Prong, Sherman
APPLICANT: APPLICANT: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/10/243,189
CURRENT APPLICATION NUMBER: US/10/3942
PRIOR APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 60/053014
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-02-4
PRIOR FILING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-10-24

PRIOR PLING DATE: 1997-11-0-24

PRIOR PLILING DATE: 1997-11-10

PRIOR PLILING DATE: 1998-03-27

PRIOR PLILING DATE: 1998-03-27

PRIOR PLILING DATE: 1998-03-27

PRIOR PLILING DATE: 1998-06-20

PRIOR PLING DATE: 1998-06-02

PRIOR PLILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/089601

PRIOR PLILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: 60/080801

PRIOR PLILING DATE: 1998-06-18

PRIOR PLILING DATE: 1998-06-28

PRIOR PLING DATE: 1998-06-25

PRIOR PLING DATE: 1998-06-25

PRIOR PLING DATE: 1998-06-25

PRIOR PLING DATE: 1998-06-25

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PRIOR PLING DATE: 1998-06-25

PRIOR PLING DATE: 1998-06-25
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3.8%; Score 104.5; DB 9;
Best Local Similarity 25.0%; Pred. No. 1.7;
Matches 53; Conservative 33; Mismatches 71;
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Publication No. US20060074033A1
GENERAL INFORMATION:
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Filvaroff, Ellen
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ORGANISM: Homo Sapien
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US-10-243-136-42
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APPLICANT:
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APPLICANT:
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Length 489;

71; DB 9;

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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PS3081C49
CURRENT APPLICATION NUMBER: US/10/243, 298
CURRENT APPLICATION NUMBER: US/10/37942
PRIOR APPLICATION NUMBER: 00/059114
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-02-47
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/086478
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                 PRIOR APPLICATION NUMBER: 60/08767
PRIOR FILING DATE: 1988-06-02
PRIOR FILING DATE: 1988-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-29
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
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PRIOR PILING DATE: 1998-06-25
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Phillippe
APPLICANT: Watanbe, Colin
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        PRIOR FILING DATE: 1998-05-22
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Matches 53; Conservative
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; ORGANISM: Homo Sapien
US-10-243-236-42
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APPLICANT:
APPLICANT:
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APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Wood, William
APPLICANT: Sang, Samin
APPLICANT: Sang, Samin
APPLICANT: Pong, Sherman
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
ITILE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PLING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/09689
PRIOR APPLICATION NUMBER: 60/09689
PRIOR APPLICATION NUMBER: 60/09689
PRIOR APPLICATION NUMBER: 60/09689
PRIOR APPLICATION NUMBER: 60/09689
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PRIOR PEDIGATION NUMBER: 60/086478

PRIOR PELING DATE: 1998-05-22

PRIOR FILING DATE: 1998-06-02

PRIOR PILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/089801

PRIOR PILING DATE: 1998-06-04

PRIOR PILING DATE: 1998-06-24

PRIOR PILING DATE: 1998-06-24

PRIOR FILING DATE: 1998-06-25

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 116
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3.8%; Score 104.5; D
Best Local Similarity 25.0%; Pred. No. 1.7;
Matches 53; Conservative 33; Mismatches
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Filvarcff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-215-42
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US-10-243-236-42
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APPLICANT: Zhang Zemin
APPLICANT: Zhang Zemin
APPLICANT: Zhang Zemin
APPLICANT: Pong, Sherman
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R1C52
CURRENT APPLICATION NUMBER: US/10/243,338
CURRENT APPLICATION NUMBER: 10/197942
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PRILING DATE: 1997-09-17
PRIOR PRILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/065027
PRIOR PRILING DATE: 1997-09-10-24
PRIOR PRILING DATE: 1998-03-27
PRIOR PRILING DATE: 1998-05-22
PRIOR PRILING DATE: 1998-06-22
PRIOR PRILING DATE: 1998-06-22
PRIOR PRILING DATE: 1998-06-22
PRIOR PRILING DATE: 1998-06-18
PRIOR PRILING DATE: 1998-06-18
PRIOR PRILING DATE: 1998-06-18
PRIOR PRILING DATE: 1998-06-18
PRIOR PRILING DATE: 1998-06-18
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          PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 42
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1 Similarity 25.0%; Pred. No. 1.7;
53; Conservative 33; Mismatches 71;
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Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean Phillippe
Watanbe, Colin
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; Publication No. US20060073579A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-304-42
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US-10-243-338-42
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 42
LENGTH: 489
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25.0%; Pred. No. 1.7;
Live 33; Mismatches
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Smith, Victoria
Srephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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Goddard, Audrey
Grimaldi, J. Christopher
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Publication No. US20060073554A1
GENERAL INFORMATION:
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US-10-243-298-42
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APPLICANT: Zong, Sherman
APPLICANT: FORGS, SHERMAN
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P36.3087LC55
CURRENT REPELICATION NUMBER: 105/10/243,357
CURRENT FILING DATE: 2002-09-13
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 42
LENGTH: 489
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PRIOR FILING DATE: 2002-07-18
PRIOR PELING DATE: 2002-07-18
PRIOR PELING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR APPLICATION NUMBER: 60/065027
PRIOR APPLICATION NUMBER: 60/066027
PRIOR APPLICATION NUMBER: 60/066478
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-05-27
PRIOR PELING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/086478
PRIOR APPLICATION NUMBER: 60/086478
PRIOR PELING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-18
PRIOR PELING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/080557
PRIOR APPLICATION NUMBER: 60/080557
PRIOR APPLICATION NUMBER: 60/090689
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
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Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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US-10-243-345-42
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APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACTOS ENCODING THE SAME
FILE REPERENCE: P3630RIC33
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                          PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
ESEQ ID NO 42
LENGTH: 489
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CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US/10/293,345

PRIOR FILING DATE: 2002-07-18

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR FILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-09-17

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-11-10

PRIOR APPLICATION NUMBER: 60/065027

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-05-22

PRIOR PILING DATE: 1998-06-02

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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
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Publication No. US20060073555A1
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Watanbe, Colin
Wood, William
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     PRIOR FILING DATE: 1998-06-24
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                       53; Conservative
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                               Similarity
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APPLICANT:
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APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watestin
APPLICANT: Watestin
APPLICANT: Weache, Colin
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Pong, Sherman
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITILE OF INVENTION: ACIDS ENCODING THE SAME
ITILE OF INVENTION: ACIDS ENCODING THE SAME
ITILE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/19/247,015
CURRENT APPLICATION NUMBER: 00/059-18
PRIOR APPLICATION NUMBER: 00/05914
PRIOR APPLICATION NUMBER: 60/05914
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/05004
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1999-05-27
PRIOR PILING DATE: 1999-06-27
PRIOR PILING DATE: 1999-06-27
PRIOR PILING DATE: 1999-06-27
PRIOR APPLICATION NUMBER: 60/08609
PRIOR PILING DATE: 1999-06-24
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3.8%; Score 104.5; I
Best Local Similarity 25.0%; Pred. No. 1.7;
Matches 53; Conservative 33; Mismatches
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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US-10-247-015-42
'Sequence 42, Application US/10247015
'Publication No. US20060073558A1
'GENERAL INFORMATION:
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                                   ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-083-42
      LENGTH: 489
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APPLICANT: Smith, Victoria
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APPLICANT: Smith, Victoria
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: Watanbe, Colin
APPLICANT: ACDIS SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING
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TITLE OF INVENTION: ACIDS
FRIOR APPLICATION NUMBER: US/10/2942
PRIOR PELING DATE: 1997-09-17
PRIOR PELING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-10
PRIOR PELING DATE: 1997-11-10
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-24
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---LHSKFWVVDGRHIYMG 211
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Grimaldi, J. Christopher
Gurney, Ausin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
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Publication No. US20060073557A1
GENERAL INFORMATION:
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Filvaroff, Ellen
NUMBER OF SEQ ID NOS: 116
                                                                                   TYPE: PRT
; ORGANISM: Homo Sapien
US-10-243-357-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-245-083-42
                         SEQ ID NO 42
LENGTH: 489
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APPLICANT:
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119 ASYYWSLTGPDIGVNDSSSQLGEALLQKLQQLLGRNISLAVATSSPTLARTSTDLQVLAA 178
                                                     380 HSGYVKYRKPL--LKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG 437
                                                                                         ||:| ::|||:|
---LHSKFWVVDGRHIYMG 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 ASYYWSLTGPDIGVNDSSSQLGEALLQKLQQLLGRNISLAVATSSPTLARTSTDLQVLAA 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Carroll, Miyoung
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
TITLE OF INVENTION: S5092 AND 10218 MOLECULES AND USES THEREFOR
FILLE REFERENCE: MPI03-0210MNIM
CURRENT FILLING DATE: 2005-09-14
PRIOR PLILING DATE: 2005-09-14
PRIOR PLILOR APPLICATION NUMBER: 09/426,282
PRIOR PLILING DATE: 1999-10-25
PRIOR PLILING DATE: 2000-09-22
PRIOR PLILING DATE: 2000-09-22
PRIOR PRILING DATE: 1999-06-11
PRIOR PLILING DATE: 1999-06-11
PRIOR PLILING DATE: 1999-06-11
PRIOR PLILING DATE: 2000-11-28
PRIOR PLILING DATE: 2000-05-16
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NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                                                                       3.8%; Score 104.5; Ilarity 25.0%; Pred. No. 1.8; Conservative 33; Mismatches
                                                                                                                                                                      438 SFNLDPRSARLNTEMGVVI-ESPKIAEQMERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 4.0
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; Sequence 15, Application US/11226701
; Publication No. US20060009632A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cook, William James
Meyers, Rachel E.
MacBeth, Kyle J.
Carroll, Joseph M.
                                                                                            :|: |: |:
179 RGAHVR-QVPMGRLTRGV--
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Williamson, Mark W.
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SEQ ID NO 15
LENGTH: 506
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US-11-226-701-15
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Best Local S
Matches 53
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                                                                                      Length 489;
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PEDLICANT: ZHANG, ZEMIN
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THE SAME
TITLE OF INVENTION: AND NUCLEIC ACIDS ENCODING THE SAME
THE REFERENCE: 39780-365381025C1
CURRENT APPLICATION NUMBER: US/11/157,996
CURRENT FILING DATE: 2005-06-20
                                                                                                                                            Indels
                                                                                                                                         71;
                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 SANMDWRSLTQVKELGAVIYNCSHLAQDLEKT 243
                                                                                ch 3.8%; Score 104.5; D. I. Similarity 25.0%; Pred. No. 1.7; 53; Conservative 33; Mismatches
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PRIOR PILLING DATE: 2002-09-11
PRIOR PILLING DATE: 2002-09-11
PRIOR PILLING DATE: 2002-09-18
PRIOR PILLING DATE: 2002-07-18
PRIOR PILLING DATE: 2001-08-29
PRIOR PILLING DATE: 2001-08-29
PRIOR PILLING DATE: 2000-02-21
PRIOR PILLING DATE: 2000-02-11
PRIOR PILLING DATE: 2000-02-11
PRIOR PILLING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 4
SEQ ID NO SEQ ID NOS: 4
LENGTH: 489
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Publication No. US20060003370A1
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SMITH, VICTORIA
WATANABE, COLIN K.
WOOD, WILLIAM I.
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GODDARD, AUDREY
GODOWSKI, PAUL J.
GURNEY, AUSTIN L.
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; ORGANISM: Homo Sapien
US-10-247-015-42
                                                                                                     Best Local Similarity
Matches 53; Conserv
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                                                                                      Query Match
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Sequence 27848, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
TATLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2756-1592PUS
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
        22;
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                                            GLSDIYLLDDPHEALAARAALIE-SAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRV 130
                                                                                                                                                                                                               173 YLTDFPRLNRRMHNKS----FTADNRATILGGRNIGDEYF-----KVGEDTVFADLDIL 222
                                                                                                                                                                                                                                                                                                                                                 266
                                                                                                                                                                                                                                                                                                                                                                                                                  267 AAGIHGDLSQARRWAVLKRFRE------GKLD-----ILVATDVAARGLD--- 305
                                                                                                                                                                                                                                                                                                       223 ATGSVVGEVSHDFDRYWASHSAHNATRII-------RSGNIGKGLQALGYN 266
                                                                                                                                                                                                                                                                                                                                                                                         267 -----DETSRHALL-RYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDR 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 RKPPIAGRLQ----DALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQA 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 YFKVGEDTV-FADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGN-----IGKGL 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 SHPNIEVRLFNPFVLRKWRALGYL-TDFPRLNRRMHNKSFTA---DNRATILGGRNIGDE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 QALGYNDETSRHALLRYRETVEQSPLYQK--IQTGRIDWQSV-----QTRLISDTPA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLL------LDDNNTRGLDDL----LLALDSHPNIEVRLFNPFVLRKWRALG
                                                                                                                                                                         114 RSLKHHVPSILVGTPGRLLDHLKRGTIDLDKVKTVVLDEADEM-------LDMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
    65; Mismatches 131; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1072;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: (1)..(1072)
; OTHER INFORMATION: Ceres Seq. ID no. 2049240
US-11-096-568A-27848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 21.23
Matches 78; Conservative
    91; Conservative
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--LHSKFWVVDGRHIYMG 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 LLDDNNTRGLDDLLLALDSHPNIEVRLFNPF----VLRKW--RALGYLTDFPRLNRRMHN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 KSFTADNRATILGGRNIGDEYF-KVGEDT---VFADLDILATGSVVGEVSHDFDRYWASH 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INCOMPATION:

APPLICANT: Klaenhammer, Todd R.

APPLICANT: Klaenhammer, Todd R.

APPLICANT: Russell, William M.

APPLICANT: Altermann, Eric

APPLICANT: McAulife, Olivia

APPLICANT: Peril, Andrea Azcarate

TITLE OF INVENTION: Nucleic Acid Sequences Encoding

TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore

FILE REFERENCE: 5051-694

CURRENT APPLICATION NUMBER: US/11/074,176

CURRENT APPLICATION NUMBER: 60/551,161

PRIOR PILING DATE: 2004-03-08

NUMBER OF SEQ ID NOS: 381

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 266

LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.8%; Score 104; DB 11; Length 328; 27.2%; Pred. No. 1; tive 28; Mismatches 88; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.8%; Score 103; DB 11; Length 495; 21.2%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                          APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53450)B EP
CURRENT APPLICATION NUMBER: US/11/087,099
CURRENT FILING DATE: 2005-03-22
NUMBER OF SEQ ID NOS: 12464
SEQ ID NO 7553
                                                                                         | | : | | | : | : | : | seanmDwrsLTQVKELGAVIYNCSHLAQDLEKT 260
                                                            SFNLDPRSARLNTEMGVVI-ESPKIAEQMERT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Streptomyces avermitilis MA-4680
US-11-087-099-7553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||| | : | : | : | SAHLAAARALTGREPGSDLTVNIGRG 252
                                                                                                                                                                                                             Sequence 7553, Application US/11087099
Publication No. US20060041961A1
GENERAL INFORMATION:
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Publication No. US20050250135A1
GENERAL INFORMATION:
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ORGANISM: Lactobacillus acidophilus
:|: |: |: |: RGAHVR-QVPMGRLTRGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 27.2*
Matches 56; Conservative
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Best Local Similarity
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US-11-087-099-7553
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APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27846
LENGTH: 1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QALGYNDETSRHALLRYRETVEQSPLYQK--IQTGRIDWQSV------QTRLISDTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            672 VTEDRD-----ALIDAAADKIEKDLILGSTAVEDKLQKGVPDCIEKLSQAGVKIWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 SHPNIEVRLFNPFVLRKWRALGYL-TDFPRLNRRMHNKSFTA---DNRATILGGRNIGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 YFKVGEDTV-FADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGN----IGKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 75;
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CORRESPONDENCE ADDRESS:
ADDRESSE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                 154;
                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (1).7 (1189)
OTHER INFORMATION: Ceres Seq. ID no. 2049238
                                                                                                                                                                                                                                                                                                                                                                                              3.7%; Score 101.5; D
21.2%; Pred. No. 12;
tive 61; Mismatches
                 ; Sequence 27846, Application US/11096568A; Publication No. US20060048240A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 85, Application US/09941095; Publication No. US20060068383A1; GENERAL INFORMATION:
APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
OLIVE, DAVID M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHOGENS
                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428 IVDGKRIFIGSFN-----
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Best Local Similarity 21.2.
The 78; Conservative
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                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION ; US-11-096-568A-27846
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US-09-941-095-85
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 27847
                                                                                               607
                                                                                                                                                                    | : : | : : | | : : | 649 --DKEAVAKASFQSIKKQLREGMSQTAAVTDNSAKENSEMFGLVIDGKSLTYALDSKLEK 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : || |: : : | | | : | | | : | | | NQPNAEL-----IQKFFRVLAIGHTAIPDVNSDTGEITYEAESPDEAAFVIASRELGFE 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : : | | : : | : : | : : | - DKEAVAKASFQSIKKQLREGMSQTAAVTDNSAKENSEMFGLVIDGKSLTYALDSKLEK 815
                                                                          INSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTF 427
                                                                                                                                                  428 IVDGKRIFIGSFN-------LDPRSARLNTEM-GVVIESPKIAEQMERTLAD 471
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KGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVP---TKSGTDALAKLVQDGIDVTVL
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; OTHER INFORMATION: Ceres Seq. ID no. 2049239
US-11-096-568A-27847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.7%; Score 101.5;
Local Similarity 21.2%; Pred. No. 11;
les 78; Conservative 61; Mismatches
                                                                                                                                                                                                                                                                                                                                                       ; Sequence 27847, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                               EFLELAIR 714
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                                   VTEDRO-
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Best Local S
Matches 78
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Query Match 3.7
Best Local Similarity 21.6
Matches 118; Conservative
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                     US-11-198-746-85
                                                                                                                                                                                                                                                          STATE: CA
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21.6%; Pred. No. 7.4;
trive 65; Mismatches 175; Indels 188;
          COMPUTER: IEM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/941,095
FILING DATE: 28-Aug-2001
CLASSIFICATION: UNMOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/941,193
FILING DATE: 28-Aug-2001
ATTORNEY/ABOTE: 28-Aug-2001
ATTORNEY/ABOTE: 28-Aug-2001
ATTORNEY/ABOTE: 28-Aug-2001
ATTORNEY/ABOTE: PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01756
TELEPHONE: (415) 705-8410
TELEPRAX: (415) 393-8338
                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ 1D NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Matches 118; Conserva
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LAVPLE 819
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118 NLMYLAAERGVRV-----RLLLDDNNTRGL---DDLLLALDS----HPNIEVRLFNPF 163
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21.6%; Pred. No. 7.4;
tive 65; Mismatches 175; Indels 188;
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF TITLE OF INVENTION: PATHOGENS
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/198,746
FILING DATE: 05-Aug-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/941,193
RILING DATE: 28-Aug-2001
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
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Sequence 85, Application US/11198746; Publication No. US20060035256A1 GENERAL INFORMATION: APPLICANT: BROW, MARY ANN D. APPLICANT: LYAMICHEV, VICTOR I. APPLICANT: OLIVE, DAVID M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: FOR TELECOMMUNICATION INFORMATION TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415) 705-8410
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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408 ----ATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESP---K 460
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                                                                                               -----LAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLW 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 KLKSTYIDPLPDLIHPRTGRLHTRPNQTATATGRLSSSDP--NLQNIPVRTPLGQRIRRA 598
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                                                                                                                                                                                                                              430 LYREVERPLSAVLAHME--ATGVRLDVAYLRALSLEVAGEIARLEAEVFRLAGHPFN--- 484
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                               164 VLRKWRALGYLTD----FPRLNRRMHNKSFT--ADNRATI-----LGGRNIGDE---
                                                                                                                                                                                                                                                                                                                                                                                                                                          EQ----SPLYQKI--QTGRIDWQSVQT----RLISDTPAKGLDRDRRKPPIAGRLQDA
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APPLICANT: BROW, MARY ANN D.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: OLIVE, DAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/11/198,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUDRESSEE: MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO STATE: CALIFORNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORS-01756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/941,193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/11/198,657
05-Aug-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 85, Application US/11198657; Publication No. US20060040299A1
                                                                                                                                                                  207 -YFKVGE--DTVFADLDILATG
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REFERENCE/DOCKET NUMBER: FOI TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-Aug-2001
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESSEE: MEDLEN & (
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PRIOR APPLICATION DATA:
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814 LAVPLE 819
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                                                                   407
                                                                                                                               ------PLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVR 705
                                                                                                                                                                                                                                               706 AWIEKTLEEGRRRGYVETLF-----GRRRYVPDLEARVKSVREAAER-MAFNMPVRGT 757
                                                                                                                                                                                              ----ATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESP---K
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3.7%; Score 101; DB 11; Length 833;
Best Local Similarity 21.6%; Pred. No. 7.4;
Matches 118; Conservative 65; Mismatches 175; Indels 18
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APPLICANT: BROW, MARY ANN D.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: LYAMICHEV, BAVID M.
TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
TITLE OF INVENTION: PATHOGENS
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
                                                               378 AVHSGYVKYRKPLLKA------GIKLYELOPNHAVP
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENT APPLICATION NATH:
APPLICATION NUMBER: US/11/198,794
FILING DATE: 05-Aug-2005
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APPLICATION NUMBER: US/09/941,193
FILING DATE: 28-Aug-2001
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 85, Application US/11198794
Publication No. US20060035257A1
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 833 amino acids
TYPE: amino acids
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MOLECULE TYPE: protein
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RESULT 39

No.11-06-568A-30808

Sequence 30808, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

TITLE OF INVENTION: Therby

CURRENT APPLICATION NUMBER: US/11/096,568A

CURRENT PILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO 30808

LENGTH: 1166
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                                                                                                                                                                                                                                                                                                                                                                                             490 DSVMFK-RLAKHGRQNERETKEHIKKYAEAGLRTLVITYREIDEDEYIVWEEEFLNAKTL 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                311 KGLDRDRRKPPIAGRLODALKOPEKSVYLVSPYFVP---TKSGTDALAKLVQDGIDVTVL 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 YFKVGEDTV-FADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGN-----IGKGL 260
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                                                                                                                                                                                           151 SHPNIEVRLFNPFVLRKWRALGYL-TDFPRLNRRMHNKSFTA---DNRATILGGRNIGDE
                                                                                                                                                                                                                        : | | : : | | : | | : | | 383 NQPNAEL-----IQKFFRVLAICHTAIPDVNSDTGEITYEAESPDEAAFVIASRELGFE
                                                                                                                                                                                                                                                                                                     602 TGDKTET---AINIGYA---CSLLREGMKQ1LVTLDSSD1EALEKQGDKEAVAKLREGMS
                                                                                                                                                                                                                                                                             207 YFKVGEDTV-FADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGN----IGKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 TNSLQATDVAAVHSGYVKYRKPLLKAGIK--LYELOPN--HAVPATKDKGLTGSSVTSLH
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                                                                                                         Length 1057;
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Best Local Similarity 21.3%; Pred. No. 12;
Best Local Similarity 21.3%; Pred. No. 12;
Marches 76; Conservative 60; Mismatches 153; Indels
                                                                                                     3.7%; Score 101; DB 11; Length 10
21.3%; Pred. No. 11;
tive 60; Mismatches 153; Indels
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  ; NAME/KEY: misc_feature
; LOCATION: (1)..(1057)
; OTHER INORMATION: Ceres Seq. ID no. 4973364
US-11-096-568A-30809
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, OTHER INFORMATION: Ceres Seq. ID no. 4973363
US-11-096-568A-30808
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                                                                                                                             Best Local Similarity 21.3 Matches 76; Conservative
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                                                                                                         Query Match
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Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 30809
LENGTH: 1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SVVGEVS-----HDFDRYW 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             330 LKQPEKSVYLVSPY-----FVPTKSGTDALAKLVQDGIDVTVLTNS-----LQATDVA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               706 AWIEKTLEEGRRRGYVETLF-----GRRRYVPDLEARVKSVREAAER-MAFNMPVRGT 757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 IAEQMERTLADTTP---EYAYRVTLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILS 517
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 ASHSAHNATRIIRSGNIGKGLQALGYNDETSRHA----------LLRYRETV
                                                                                                                                                                                                                                                                                                                                                                                                  164 VLRKWRALGYLTD----FPRLNRRMHNKSFT--ADNRATI------LGGRNIGDE----
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                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                            3.7%; Score 101; DB 11; Length 833;
21.6%; Pred. No. 7.4;
tive 65; Mismatches 175; Indels 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 -YFKVGE--DTVFADLDILATG-----
               TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 833 amino acids
TYPE: amino acid
STRANDEDNESS: single
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ORGANISM: Arabidopsis thaliana
(415) 705-8410
                                                                                                                                                                                                                          3.74
Query Match
Best Local Similarity 21.69
Matches 118; Conservative
                                                                                                                                           TOPOLOGY: linear
HOLECULE TYPE: protein
US-11-198-657-85
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LAVPLE 819
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TELEPHONE:
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUG2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 30807
||| : || | : || : || 658 VTEDRD-----ALIDAAADKIEKDLILLGSTAVEDKLQKGVPDCIEKLSQAGVKIWVL 710
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; OTHER INFORMATION: Ceres Seq. ID no. 4973362
US-11-096-568A-30807
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Job time : 31 secs
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ORGANISM: Arabidopsis thaliana
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US-11-096-568A-30807
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05-JUL-2004 (TEMBLEE1, 27,
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Maximum Match 100%
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MEDLINE=22935225, PubMed=14573659;

XX DOI=10.1128/AIT.11.11.6381-6391.2003;

MEDLINE=22935225, PubMed=14573659;

XX DOI=10.1128/AIT.11.11.6381-6391.2003;

BEGWARGS J.L., BRIZ D.D., Apical M.A.;

"Gonococcal phospholipase d modulates the expression and function of complement receptor 3 in primary cervical epithelial cells.";

Infect. Immun. 71:6381-6391(2003).

REMBL; AY307929; AAQ77232.1; -; Genomic DNA.

GO; GO:0003824; F:catalytic activity; TEA.

RO; GO:0003824; F:catalytic activity; TEA.

R InterPro; IPR001736; PLD.

R Ffam; PF00614; PLDc; 2.

R SMART; SM00155; PLDc; 2.

R RNART; SM00155; PLDc; 2.

R RNART; SM00155; PLDc; 2.

R RNART; SM00155; PLDc; 2.

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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Phospholipase D (Fragment).
Name-pld,
Neisseria gonorrhoeae.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriaceae; Neisseriaceae; Neisseriae.
NCBI _TaxID=485;
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100.0%; Pred. No. 7.6e-184;
ive 0; Mismatches 0;
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098NZ3_RHILO
088RZ3_ACRYS
0984B3_RHILO
06FB53_ACIAD
06DE243_BURMA
086CAS_BEBAR
041JD9_9BURK
041JJ3_BURPS
061JJ3_BURPS
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421 SLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRV
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                                                                                                                                       SLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=22491 / Serogroup A / Serotype 4A;
MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Dovlin K., Feltwell T., Hamlin N., Holroyd S.,
Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis 22491.";
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                                                           GIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVT
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.2%; Score 2643; DB 2;
97.3%; Pred. No. 2.1e-178;
ive 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mature 404:502-556(2000).

EMBL, AL167756; CAB84874.1; -; Genomic_DNA.

PIN, B81859; B81859.

GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro: IRF001736; P.D.

SPÉam; FSF00614; PLDC; 2.

SMART; SM00155; PLDC; 2.
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OrderedLocusNames=NMA1646;
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SEQUENCE 525 AA
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    SHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSV 300
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                                                               GIDVTVLTNSLQATDVAAVHSGYVKYRRPLLKAGIKLYELQPNHAVPATKDKGLTGSSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Lewis L.A., Gillaspy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,

Lownbey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,

Song L., Lin S., Yuan X., Nydick C., Carson M.B., Vaughn J., Thomson C.,

Kenton S.M., Lai H., White J.D., Clifton S., Ree B.A., Dyer D.W.;

Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AE004969; AAW89600.1; -; Genomic_DNA.

InterPro; IPR001736; PLD.

SMART; SM00155; PLDC, 2.

SMART; SM00155; PLDC, 2.

PROSITE; PSS0035; PLD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MHTDPKIQAMPSETISPMKTRSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ILQIRHTPHNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVT
                                                                                                                                                                                                    SLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRV
                                                                                                                                                                                                                                         SLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRV
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Putative phopholipase D-family protein.
OrderedLocusNames=NGO0902,
OrderedLocusNames=NGO0902,
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
Neisseriaceae, Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.7%; Score 2712; DB 2; 99.6%; Pred. No. 2.8e-183;
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QSF887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523; Conservative
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Best Local Similarity
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Matches
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360 437 420 497

317 300 480

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RETAIN—Toblama I / ATC BAA-589 / NCTC 13251;

X MDDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

X PATAIN—Toblama I / ATCC BAA-589 / NCTC 10.1038/ng1227;

X PATAIN — 1. Sebahia M., Preston A., Murphy L.D., Thomson N.R.,

XA Harris D.E., Holden M.T.G., Churcher C.M., Bencley S.D., Mungall K.L.,

XA Achtman M., Atkin R., Baker S., Basham D., Baron N., Cherevach I.,

XA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

XA Chillingworth E., Noules S., Norberczak H., Holroyd S., Jagels K.,

X Laather S., Moules S., Norberczak H., O'Neill S., Ormond D., Price C.,

XA Babbinowitsch E., Rutter S., Sanders M., Saunders D., Price C.,

XA Babbinowitsch E., Rutter S., Sanders M., Saunders D., Price C.,

XA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

XI "Comparative analysis of the genome sequences of Bordetella pertussis,

RT "Comparative analysis of the genome sequences of Bordetella pertussis,

RT Genet. 35:32-40(203).

RO; GO:0003824; F:catalytic activity; TEA.

RG GO: GO:0003824; F:catalytic activity; TEA.
                                                                                                                                                                         RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA
                                                                                                                                                                                                                                                                                                                                                                                             361 AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRLQWHDPATRK
                                                                                                                                            LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG
                                                                                                                                                                                                                                                      KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLITE]. 25, Created)
01-MAR-2004 (TrEMBLITE]. 26, Last sequence update)
Putative phospholipase D protein.
OrderedLocusNames=BP3092;
Bacterila pertussia
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48.6%; Pred. No. 5.8e-75;
tive 77; Mismatches 152;
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Q7VUJ6;
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Best Local Similarity 48.64
Matches 258; Conservative
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PROSITE; PS50035; PLD; 2.
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SEQUENCE 524 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-2017575; PubMed=10710307; DOI=10.1126/science.287.5459.1809; MEDLINE-20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809; Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D., Hork P.W., Mile O., Fleischmann R.D., Dougherty B.A., Mason T.W., Ciecko A., Parksey D.S., Blair B., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M., Olin H., Vamathevan J.J., Gill J., Scarlato V., Masignani V., Pizza M., Venter J.C., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of Neisseria meningitidis serogroup B strain
                               QTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQD
                                                                                                                                                                                                                 GIDVIVLINSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLIGSSVT
                                                                                                                                                                                                                                                   GIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVT
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SHSAHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSV
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Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cardiolipin synthetase family protein.
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Pred. No. 1.8e-173;
5; Mismatches 6;
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GO, GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001736; PLD.
Fram; PP00614; PLDc; 2.
SMART; SM00155; PLDc; 2.
PROSITE; PS50035; PLD; 2.
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Science 287:1809-1815(2000)
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Q9JYUO;
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NCBI_TaxID=491;
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SEQUENCE 508 AA;
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SMART; SM00155; PLDc; 2. PROSITE; PSS0035; PLD; 2. Complete proteome. SEQUENCE 492 AA; 53309
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                                                                                                             KSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHN 246
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                                                                                                                                                              AGPLLPA----PGAQTLRALAERAARIEQDPAAGDYMSALRELPFIRELMAGRLPLQWAP
                                                                                                                                                                                                                           --HNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAER
                                                                                     GVRVRLLLLDDNGISGLDDALAALDAHPNAEVRLFNPFPTRSFKALGYLTDFSRLNRRMHN
                                                                                                                                              ATRIIRSGNIGKGLQALGYNDETSRH-----ALLRYRETVEQSPLYQKIQTGRIDWQSVQ
                                                                                                                                                                               TRLISDTPAKGLDRDRRKPPIAG----RLQDALKQPEKSVYLVSPYFVPTKSGTDALAKL
                                                                                                                                                                                                                  358 VQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGS
                                                                                                                                                                                                                                                                                             OrderedLocusNames=BB0822;
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
         KTRSLISL - - LCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDNILQIRHTP -
                                                                                                                                                                                                                                                                                    YRVTLDKHNRLQW----HDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL
                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative phospholipase D protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nat. Genet. 35:32-40(2003).

EMBL; BX640439; CAE31321.1; -; Genomic_DNA.

GO; GO:0003824; F:catalytic activity; TEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR001136; P.D.

Pfam; PF00614; PLDC; 2.
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Q7wp63;
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                                                                                                                                                                                                                                                                                 172 FGATDGVLFADLDVLAVGPVVGDVSAEFDAYWASESAWPAGPLLPA----PGAQTLRALA 227
                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                -----YLLDDPHEALA
                                                                                                                                                                             88 ARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLDDLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 ALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNIGDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 VHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGS
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MEDLINE=238824; PubMed=12471157; DOI=10.1073/pnas.252529799;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Mctensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli..;
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

EMBL; AE016759; AAN79783:1; -; Genomic DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                 Gaps
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                                                                                                 40;
                                                 Length 492;
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BC6BFEE8AC34E726 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein ymdC.
Name=ymdC; OrderedLocusNames=c1310;
                                                                                                                                                   38 LPPLEERTESRHFNTSKPVLLDNILQIRHTPHNNGLSDI-
                                            43.4%; Score 1181; DB 2;
49.6%; Pred. No. 6.3e-75;
tive 70; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 RKTYPNEPEAKLWKRIAAKILSLLPIEGLL
492 AA; 53309 MW;
                                                                                                 Matches 253; Conservative
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MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glaaner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                           40.6%; Score 1104.5; DB 2; Length 493; 47.5%; Pred. No. 1.6e-69; Live 85; Mismatches 143; Indels 15;
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                                                                                                                                                                                                                                                                                                                                       143; Indels
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GO; GO:0008654; P:phospholipid biosynthesis; IEA.
Interpro; IPR001736; PLD.
Pfam; PF00614; PLDc; 2.
SMART; SM00155; PLDc; 2.
PROSITE; PS50035; PLD; 2.
COMPIET; PS50035; PLD; 2.
COMPIET; PS50035; PLD; 3.
COMPIET; PS50035; PLD; 3.
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
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01-NOV-1997 (Rel. 35, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
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Name=ymdC; OrderedLocusNames=b1046;
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MEDLINE=97061202; PubMed=8905232;
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Matches 220; Conservative
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Mau B., Shao Y.;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Kikmura C., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Sampei G., Seki Y., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T., "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map."; PNA Res. 3:13-155(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome; Hypothetical protein; Repeat; Transferase.

DOMAIN 145 172 PLD phosphodiesterase 1.

DOMAIN 384 411 PLD phosphodiesterase 2.

SEQUENCE 493 AA; 55927 MW; 495604ADBDBD8492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 2 PLD phosphodiesterase domains.
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EMBL, D90741; BAA35836.1; -; Genomic_DNA.
EMBL, D90742; BAA35844.1; -; Genomic_DNA.
PIR, C64847; C64847.
EchoBASE, EB3634; -.
EcoGene; E013875; ymdc.
InterPro, IPR001736; PLD.
Pfam; PF00614; PLDc; 2.
SMART; SM00155; PLDc; 2.
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390 AKTFSIDGKTVFIGSFNFDPRSTLLNTEMGFVIESETLAQLIDKRFIQSQYDAAWQLRLD 449
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                       AKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLD 483
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MEDLINE=21156211; PubMed=11258796;
MEDLINE=21156211; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
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                                                                                                                    484 KHNRLQWHDPATRK--TYPNEPEAKLWKRIAAKILSLLPIEGLL
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Last sequence update)
Last annotation update)
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EMBL: BADGNOO7; BAB34847.1; -; Genomic DNA. GO; GO:0003824; F:catalytic activity; EA. GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Escherichia
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Pfam; PF00614; PLDc; 2.
SWART; SMO0155; PLDc; 2.
PROSTIE; PSS0035; PLD; 2.
SEQUENCE 493 AA; 55928 M
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Matches 220; Conservative
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Q7AFA8_ECO57_PRELIMINARY;
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                       STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Jin O., Yang F., Zhang X., Zhang J., Yang G., Wu H., Ou D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Yu J.;
"Genome sequence of Shigella flexneri 2a: insights into pathogenicity
"Lthrough comparison with genomes of Escherichia coli K12 and O157.";
Nucleic Acids Res. 30:4432-4441(2002).
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STRAIN=2457T / ATCC 700930 / Serotype 2a;

MEDLINE=22590274; PubMed=12704152;

DOI=10.1128/IAI.71.5.2775-2786.2003;

A Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

A Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Dang W.,

A Rourhier G., Mayhew G.P., Plunkett G. III, Rose D.J., Darling A.,

A Schwartz D.C., Blattner F.R.;

"Complete genome sequence and comparative genomics of Shigella

"I lexneri serotype 2a strain 2457T.";

II nfect. Immun. 71:2775-2786(2003).

EMBL; AE016981; AAP16548.1; -; Genomic_DNA.

EMBL; AE016981; AAP16548.1; -; Genomic_DNA.

EMBL; AE016981; AAP16548.1; -; Genomic_DNA.

GO; GO:0003824; F:catalytic activity; IEA.
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                                          01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
11-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Putative synthase.
Name=ymdC; OrderedLocusNames=S1116, SF1042;
Shigella flexneri.
       493 AA
                                                                                                                                                                                       Bacteria, Proteobacteria, Gar
Enterobacteriaceae, Shigella
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Q83RUS SHIFL PRELIMINARY;
Q83RUS; Q7UCY8;
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PROSITE; PS50035; PLD; 2.
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SEQUENCE 493 AA;
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"The genome sequence of Salmonella enterica serovar Choleraesuis, highly invasive and resistant zoonotic pathogen.";

Nucleic Acids Res. 33:1690-1698(2005).

Res. AAX65001.1; -; Genomic_DNA.

Complete proteome.

SEQUENCE 528 AA; 60029 MW; D5175EE93D71CBDB CRC64;
                                                                                                                                                                                                                                                                                                                                                Salmonella cholerae-suis (Salmonella enterica).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
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10-WAY-2005 (TrEMBLrel. 30, Last sequence update)
10-WAY-2005 (TrEMBLrel. 30, Last annotation update)
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Matches 235; Conservative
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X STRAIN-0157-H7 / ED1933 C STRAIN-0157-H7 / ED1933 C STRAIN-0157-H7 / ED1935; PubMed=11206551; DOI=10.1038/35054089;

X Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

X Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

X Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

KI Mature 409:259-533(2001).

NR PIR, D85666, D85666.

PIR, H90806, H90806.
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                                                                                 Last sequence update)
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                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001736; PLD.
SMART; SM00155; PLDC; 2.
                                                          Created)
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Name-ymdC, OrderedLocusNames=z1680, Escherichia coli 0157:H7.
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Q8X917_ECO57 PRELIMINARY;
Q8X917;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDR 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 LISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLLDNILQIRH-----TPHNNGLSDIY
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MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;

MAND B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;

"Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:346-3465(2001).

EMBL; AE006196; AAK03670.1; -; Genomic DNA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0008152; Piemetabolism; IEA.

PFO0614; PLDC; 2.
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                                                                                                                                                                                                                                                                                                       Pasteurella multocida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
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514 AA; 57882 MW; C65B0EB65DB0F216 CRC64;
                                                                                                                                                                        Last sequence update)
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein PMIS86.
OrderedLocusNames=PMI586;
                                                                  QGCKMS_PASMU PRELIMINARY;
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PROSITE; PS50035; PLD; 2.
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                                                                                                                                                                                                                                                                                             MEDLINE=2134948; PubMed=11677609; DOI=10.1038/35101614;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Green IN., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
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"Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 GLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVR
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                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.1%; Score 1089.5; DB 2; Length 494; 47.4%; Pred. No. 1.9e-68; Live 77; Mismatches 147; Indels 21;
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                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AE008149; AAL20078.1; -; Genomic_DNA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:001740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008654; P:phospholipid biosynthesis; IEA.
InterPro; IPR001736; PLD.
FAMT; PR00614; PLDC; 2.
SMART; SMO0155; PLDC; 2.
PROSITE; PS50035; PLD; 2.
  494
                                                                                                       Putative phospholipase.
Name-ymdC; OrderedLocusNames=STM1148;
Salmonella typhimurium.
PRT;
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                                                                                                                                                                                                   Enterobacteriaceae; Salmonella
QBZQ28 SALTY PRELIMINARY;
Q8ZQ28;
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Matches 221; Conservative
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                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                      NCBI_TaxID=602;
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Enterobacteriaceae; Salmonella.
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QSPGY9;
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"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Dong W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
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                                                                                                                                                                                        Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.1%; Score 1089.5; DB 2; Length
47.4%; Pred. No. 1.9e-68;
tive 77; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                       MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
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SEQUENCE 495 AA; 56348 MW; 4555257D8DD83AB9 CRC64;
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EMBL; AL627269; CAD08272.1; -; Genomic_DNA.
EMBL; AE016840; AA069395.1; -; Genomic_DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0018122; P:metabolism; IEA.
GO; GO:0008122; P:metabolism; IEA.
GO; GO:0008614; P:metabolism; IEA.
Ffam; PF00614; PLDc; 2.
EMBL; SM00155; PLDc; 2.
QBZ7MO_SALTI PRELIMINARY; PRT; 495 AA.
QBZ7MO; Q7C9A7;
01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
10-PEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein STY1185.
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PROSITE; PS50035; PLD; 2
                                                                                                                                                                                                                                                                                          SEQUENCE.
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                                                                                                                                                                    Salmonella typhi.
                                                                                                                                                                                                                                        NCBI_TaxID=601;
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SEQUENCE 495 AA; 56310 MW; 8BAADE58874983A2 CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein ymdC.
Name-ymdC; OrderedLocusNames=SPA1703;
Salmonella paratyphi-a.
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                                                                                                                                                                                                                         LVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQP-----NHA 405
LLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDDN
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US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
NCBI_TaxID=331272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which
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Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
hospholipase D/ransphosphatidylase precursor.
ORFNames=Bcen2424DRAFT 3266;
Burkholderia cenocepacia H12424.
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US DOB Joint Genome Institute (JGI-ORNL);
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Q4LR64;
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NUCLEOTIDE SEQUENCE.
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NUCLEOTIDE SEQUENCE.
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                                                                RLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGI 362
                                                                                                                             270 RLLSDDPSKGEGKAQRHSLLPQRLFDVMGSPTERIDIISAYFVPTRAGVAQLLNLVRKGV 329
   SLSE----QELTQRIELPESWYNDEITR----RYLHKLETSQFMADLDCGTLPLIWAKT 269
                                                                                                                                                                                                 363 DVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHA-VPATKDKGLTGSSVTS 421
                                                                                                                                                                                                                                                                                                                               LHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVT 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acinetobacter sp. (strain ADP1).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
NCBI_TaxID=62977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDKHNRLQWHD--PATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 KGLQALGYNDETSRHALLRYRETVEQ-SPLYQKIQTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative phospholipase D protein.
OrderedLocusNames=ACIAD3001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 34.6%; Score 940.5; DB 2; al Similarity 38.2%; Pred. No. 7.2e-58; 207; Conservative 101; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519 AA; 59913 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEFBA6_ACIAD PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
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SEQUENCE 519 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                482
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                                                                                189 FTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNA-
                                                                                                                                                                                55 DPKTITGFYPLNQGHDALLARTSLIESAQKSLDLQYYIYRGDETSQLITWRLYEAAKRGV
                                                 129 RVRLLLDDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKS
                                                                                                                                                                                                                                                      -----TRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSV
                                                                                                                                                                                                                                                                                                     232 MEWISPQSQSVSDAAIQKQVTKLNLQEKFSSG---RYDFTA--LDMYQDLKQGKLNLYWG
                                                                                                                                                                                                                                                                                                                                                   QTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDK-GLTGSSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | : | : | : | : | : | : | : | : | RVLVVASCFGELTAKYYEQLRPETVKDNLTGFHSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.;

Choy H.E.;

"Complete genome sequence of Vibrio vulnificus CMCP6.";

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AE016810; AA007638.1; -; Genomic_DNA.

GO; GO:0016740; Fitzansferase activity; IEA.

InterPro; IPR001736; PLD.

Ffam; PF00641; PLDC; 2.

SMART; SM00155; PLDC; 2.

PROSITE: PS50035; PLD; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Phosphatidylserine/phosphatidylglycerophosphate/ cardiolipin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio vulnificus.

Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio.

Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.1%; Score 872.5; DB 2; Length 39.1%; Pred. No. 4.5e-53; Live 89; Mismatches 211; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480 VTLDKHNRLQWHDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=VV20702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBD641_VIBVU PRELIMINARY;
Q8D641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 39.1 nes 198; Conservative
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W NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

W NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

C STRAIN=RIMD 2210633 / Serctype 03:KG.

W MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

M Aijima Y., Najima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

A Ijijua Y., Najima M., Nakano M., Yamashira A., Kubota Y., Kimura S.,

A Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

RT Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism R distinct from that of V. cholerae.";

RG Ennet 361:743-749(203).

DR GO; GO:0008182; F:catalytic activity; IEA.

DR GO; GO:0008182; P:metabolism; IEA.

DR Hom; PF00614; PLDC; 2.

DR FAm; PF00614; PLDC; 2.

DR SARRY; SMO0155; PLDC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 TPAK----GLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGID 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         424 AKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLD 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128
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                                              NTRGLDDLLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI
                                                                                                                       LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG
                                                                                                                                                                                                                       KGLQALGYNDETSRHALLRYRETVEQSPLY----QKI-----QTGRIDWQSVQTRLISD
                                                                                                                                                                                                                                                                           241 GGL-----ERERERLRDYLRAMEDNPYVLEARQRLDRIVHGOGTELSWG--HATVLYD
                                                                                                                                                                                                                                                                                                                                                                                                                         VIVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDPAGSGRLKWVQTDADGKVTEIDHEPEVSAPRRMEVWFLGLFPIESQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 K----HNRLOW--HDPATRKT-YPNEPEAKLWKRIAAKILSLLPIEGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome, Hypothetical protein.
SEQUENCE 505 AA; 57220 MW; 362B9C2947F2446F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUNAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein VPA0341.
OrderedLocusNames=VPA0341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       505
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Matches 208; Conservative
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                    138
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                                                                                                                                                  FDLÝWNSLHAVPIEWLTDNPIPVTE----EBĽÓA--WLKETQLEQKFTQGRYDFTQLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                        292 YÓQFTDKSLVWYWGKGQVWYDLPDK---VDTQAPQLADNLASLLRTVKDSLVLISPYFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAV
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                                                                                                                                                                                                                                        FDRYWASHSA------HNATRIIRSGNIGKGLQALGYNDETS-RHALLRYRETVEQSPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=14656965; DOI=10.1101/gr.1295503; Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C., Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.; Comparative genome analysis of Vibrio vulnificus, a marine pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio vulnificus (strain YJO16).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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SEQUENCE 554 AA; 63341 MW; 8A7980BB096AB6C8 CRC64;
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Last sequence update)
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EMBL, BA000037; BAC93923.1; -; Genomic DNA.

GO; GO:0003824; F:catalytic activity; ĪEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR001736; PLD.
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PROSITE; PS50035; PLD;
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Matches 207; Conserv
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                                                                         KPPIAGRIQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVAA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGS 438
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                                                                                                                                                                      GRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKG
                                                                                                                                                                                                                                     181 GRNIGNEYFSFSTQVEFGDFDVLLFGPAVVETATQFDLYWNSDQTQSVSALVSLSDYETQ
                                                                                                                                                                                                                                                                                                          260 LQALGYNDETSRHALLRYRE-TVEQSPLYQKIQTGRIDWQSVQTRLISDTPAKGLDRDRR
                                                                                                                                                                                                                                                                                                                                                                         241 YALEDLVDVNALEAPFRDGEYDISQLELFEHLKHGTLKLYWGEAVLWYDLPDKVETRDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PKIQAMPSETISPMKT---RSLISLLCLLLCSCSSWLPPLEERTESRHFNTSKPVLL---
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Choy H.E.;
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Vibrionaceae; Vibrio.
VCBI_TaxID=672;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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larity 39.4%; Pred. No. 5.6e-53;
Conservative 89; Mismatches 197;
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YDSEPESSIWRSIGAWLSGVLPIEGML 501
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Phopholipase D-family protein.
OrderedLocusNames=VV13126;
Vibrio vulnificus.
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Q8D861;
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STRAIN=306 / ACCT 13902 / XV 101;

WEDLINE=22022145; PubMed=12024217; DOI=10.1038/4174599;

A Guaggio R. B., Monteiro-Vitorello C. B., Van Sluys M.A.,

A Quaggio R. B., Monteiro-Vitorello C. B., Van Sluys M.A.,

Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,

A Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,

B L-Dorry H., Faria J.B., Ferraira A.J.S., Ferreira R.C.C.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemose B.G.M., Lemos M.V.F.,

Moreira L.M., Novo M.T.M., Marchado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V. K., Oliveira M.C., Oliveira V.R.,

Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

"Comparison of the genomes of two Xanthomonas pathogens with differing that specificities."
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      RGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILG 199
                                                                                                                                                                                                                                                                                                                                          LINSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKT 426
                          GRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIGKG
                                                                                                                                                                                                    260 LQALGYNDETSRHAL-----LRYRE---TVEQSPLYQKIQTGRIDWQSVQTRLIS
                                                                                                                                                                                                                                                         DTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTV
                                                                                                                                                                                                                                                                                                                                                                                                                              427 FIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEOMERTLADTTPEYAYRVTLDKHN
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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Last sequence update)
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EMBL; AB011929; AAM37716.1; -; Genomic DNA.

GO; GO:0003824; F:catalytic activity; ĪEA.

GO; GO:0008152; P:metabolism; IEA.

InterPro; IPRO01736; PLD.

PHAM: PF006114; PLDC; 2.

SMART; SM00155; PLDC; 2.

COMDlete proteome.

SEQUENCE 520 AA; 57436 MW; 61A2DE5E0349A2
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01-MAR-2004 (TrEMBLrel.
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Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio vulnificus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Phopholipase D-family protein.
OrderedLocusNames=VV13197;
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                                                                                                    QAHADQ----TGMVILPDNVDAFAVRALTARAAGRSLDLQYYIWHADFTGNLLHNELLRA 116
                                                                                                                                        TG--RIDWQSVQTRLISDTPAKG----LDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFV 345
                                                                                                                                                                                                                                                                                         PTKSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHA 405
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                                                                                                                             AERGVRVRLLLLDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRK---WRALGYLTDFPRL
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                              Gaps
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PubMed=14752164; DOI=10.1126/science.1093027;
Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C., Keller H., Lambert C., Favns K.J., Goesmann A., Meyer F., Sockett R.E., Schuster S.C.;
"A predator unmasked: life cycle of Bdellovibrio bacteriovorus from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
Bdellovibrionaceae; Bdellovibrio.
                             75;
         Length 520;
                            Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
        31.3%; Score 850.5; DB 2; 37.9%; Pred. No. 1.7e-51; ive 80; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic perspective.";
Science 303:689-692(2004).
EMBL; BX842647; CAE78430.1; -; Genomic DNA.
GO; GO:0003824; F:catalytic activity; ĪEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001736; PLD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 530
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OrderedLocusNames=Bd0448;
Bdellovibrio bacteriovorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           206; Conservative
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          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRDRRKPPIAGRIQDALKQPEKSVYLVSPYPVPTKSGTDALAKLVQDGIDVTVLTNSLQA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDVAAVHSGYVKYRKPILKAGIKLYELQPNHAVPATKDKGLTGSSVTS--LHAKTFIVDG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPEYAYRVTLDKHNRLQW- 490
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Ayala-del-Rio H.L., Chain P., Ponder M.A., Di Bartolo G., Ivanova N.,
Bergholz P.W., Hauser L., Land M., Bakermans C., Rodrigues D.,
Klappenbach J.A., Zarka D., Larimer F., Richardson P., Thomashow M.F.,
Tiedje J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 YEKGLAILDYHPNVEVRMANPPAGRTWKILDAMR-FSTVNRRMHNKVFVVDNQTAIVGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 ALGYNDETSRHAL-----LRYRETVEQSPLYQKI--QTGRIDWQSVQTRLISDTPAK-GL
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                                                                                                                                                                                                                                                       24 ISLLCLLLCSCSSWLPPLEER--TESRHFNTSKPVLLDNILQIRHTPHNNGLSDIYLLDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 LDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGR
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ORFUMAMES=PSOC 0791;

Psychrobacter arcticum 273-4.

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                        25;
                                                                                                                                                      Length
                                                                                                                                                                                                        Indels
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Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                      4C810BFAFD934F6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 31, Created)
(TrEMBLrel. 31, Last sequence update)
(TrEMBLrel. 31, Last annotation update)
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                                                                                                                                                      Score 849.5; DB 2;
Pred. No. 2.1e-51;
                                                                                                                                                                                                        84; Mismatches 205;
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                                                                               Potential
                                                                                                      530 AA; 59501 MW;
                                                                                                                                                      31.2%;
SMART; SM00155; PLDC; 2. PROSITE; PS50035; PLD; 2. Complete proteome; Signal. SIGNAL
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Q4FTL4;
                                                                                                                                                                                                           Matches 203; Conservative
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NUCLEOTIDE SEQUENCE
                                                                                                                                                                                Similarity
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78 LLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDN 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | :::|:|||| |||||::||| | |::||364 VIVDSEKVFVGSFNFDPRSAQINTESGLLIESAEMAERINAMFEHELFLRSYEARLNRFY 423
                                                                                                                                                                                                                  74
                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 DPLKALPDSKPSRLVTQQLTQTLGLAKQSIVLVSPYFVPTPTGVKELENLSEQGVKVRVL
                                                                                                                                                                                                                                                                                                                              SSDKPRLFND-----IWKGYQKQPELRDLHQFVLSDEHLTDTPQSDAETWYQATATVVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI
                                                                                                                                                                                                                                                                 LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TPAKGLDRDRRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKD-KGLTGSSVTSLHAKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria pv. campestris str. 8004.
Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=314565;
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                                                                                                                         Length 464;
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40.4%; Pred. No. 5.8e-51;
ive 71; Mismatches 174; Indels
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VCE 520 AA; 57165 MW; 8849CFED240410A3 CRC64;
                                                                                            59A8BFA13DEB45F7 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                       31.1%; Score 846; DB 2; L
40.2%; Pred. No. 3e-51;
tive 76; Mismatches 173;
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Xanthomonas campestris pv. campestris
    IEA
    GO:0008152; P:metabolism;
                                                                                            464 AA; 53557 MW;
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 GO; GO:0008152; P:metabol:
InterPro; IPR001736; PLD.
Pfam; PF00614; PLDC; 2.
SMART; SM00155; PLDC; 2.
                                                                                                                         Query Match
Best Local Similarity 40.23
Matches 186; Conservative
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Q4UWU7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 40.4
Matches 196; Conservative
                                                              PROSITE; PS50035; PLD; 2
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ORFNames=XC 1408;
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                                                                              Complete proteome.
SEQUENCE 464 AA
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Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNSLQATDVA 377
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                                                                                                                                                                                                   ALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDD-NNTRGLD
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AVHSGYSQWRPSLLRAGVKIYELKSTASEEKRENKLWKGRSQSSTSLHAKAFAVDDYQVF
            Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Chain P., Di Bartolo G., Ivanova N., Hauser L., Land M., Larimer F., Pitluck S., Richardson P., Submitted (JUN-2005) to the EMBL/Genbank/DDBJ databases.

EMBL; CP000082; AAZ18644.1; -; Genomic DNA.

SEQUENCE 570 AA; 63466 MW; OECC7DAĀ9ECA3BCI CRC64;
                                                                                                                                                                                                                                             144 DLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATILGGRNI
                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=L2-TR / DSM 15497 / ATCC BAA-735;
PUDMed=15596722; DOI=10.1073/pnas.0407638102;
Hou S., Saw J.H., Lee K.S., Freitas T.A., Belisle C., Kawarabayasi
Donachie S.P., Pikina A., Galperin M.Y., Koonin E.V., Makarova K.S.
Omelchenko M.V., Sorokin A., Wolf Y.I., Li Q.X., Keum Y.S.,
Campbell S., Denery J., Aizawa S.-I., Shibata S., Malahoff A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the deep-sea gamma-proteobacterium Idiomarina
loihiensis reveals amino acid fermentation as a source of carbon
                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Idiomarinaceae; Idiomarina.
NCBI_TaxID=135577;
                                                                                                                         Length
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 101:18036-18041(2004)
EMBL; AE017340; AAV82284.1; -; Genomic DNA.
GO; GO:0003824; F:catalytic activity; TEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                    31.2%; Score 848.5; DB 2;
40.0%; Pred. No. 2.7e-51;
iive 87; Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494 ATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKKVIYDSEPRVAVSDHVWLTIMSWLPIDWLL
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01-FEB-2005 (TrEMBLrel. 29, Last
01-FEB-2005 (TrEMBLrel. 29, Last
Phospholipase D family protein.
OrderedLocusNames=IL1444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSQUYB IDILO PRELIMINARY;
QSQUYB;
                                                                                                                                                    Matches 181; Conservative
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                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                    259 (
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                                                                                                                       Query Match
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                                                                                                                                        Local
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EMBL; AE012383; AAM41978.1; -; Genomic DNA.
GO; GO:0003824; F:catalytic activity; ĪEA.
GO; GO:0008152; P:metabolism; IEA.
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OrderedLocusNames=BQ01680;
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QGG185;
                                                                  InterPro; IPR001736; PLD. Pfam; PF00614; PLDc; 2.
                                                                                                                                                                                                                                                                             Matches 196; Conservative
                                                                                                             SMART; SM00155; PLDC; 2.
PROSITE; PS50035; PLD; 2.
                                                                                                                                                             Complete proteome. SEQUENCE 520 AA;
                                                                                                                                                                                                                                                       Similarity
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WEDLINE-22022145; PubMed=12024217; DOI=10.1038/417459a;

Ma Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,

Camarot L.B.A., Camarotte G., Cannavan F., Cardoxo J., Chambergo F.,

Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,

R. Ciapina L.P., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

Restoyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Locali B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.A., Manck C.F.M., Miyaki C.Y., Moon D.H.,

Mortins E.C., Maddanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

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Mortins L.M., Novo M.T.M., Okura V.K., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Comparison of the genomes of two Xanthomonas pathogens with differing
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                                                                                                                                                                                                                                                                                                                                                                                           290 IOTGR--IDWQSVQTRLISDTPAKG----LDRDRRKPPIAGRLQDALKQPEKSVYLVSPY
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Q8P7A5;
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Cardiolipin synthase.
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                            122 LAAERGVRVRLLLDDNNTRGLDDLLLALDSHPNIEVRLFNPFVLRK---WRALGYLTDFP
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STRAIN=TOULOuse;
PubMed=15210978;
PubMed=15210978;
Prank A.C., Karlberg E.O., Legault B.-A., Ardell D.H
Canback B., Eriksson A.-S., Nacslund A.K., Handley S.A., Huvet M.,
La Scola B., Holmberg M., Andersson S.G.E.,
"The louse-borne human pathogen Bartonella quintana is a genomic
derivative of the zoonotic agent Bartonella henselae.";
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                                                      Length 520
                                                                                                      Indels
520 AA; 57165 MW; 8849CFED240410A3 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                31.0%; Score 843; DB 2; Le
40.4%; Pred. No. 5.8e-51;
ive 71; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bartonella quintana (Rochalimaea quintana)
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GO:0008152; P:metabolism; IEA
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                                                            Complete proteome
SEQUENCE 523 AA
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                                                                                                                                                                                                                                                                                   261 QALGYNDETSRHALLRYRET-VEQSPL-YQK-----IQTGRIDWQSVQTRLISDTPA 310
                                                                                                                                                                                                                                                                                                                                     KGLDRDRRKPPIAGR-LQDALKQ----PEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVT 365
                                                                                                                                                                                                                                                                                                                                                                                                                              310 KAL---RKK---AĞNWİMKALSOVIGDAQKTVQITSPYFVPGKVGTQSFRNLVSKGVDVK 363
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WUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN-ATCC 49882 / Houston 1;

PubMed=15210978; DOI=10.1073/pnas.0305659101;

Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell D.H.,

Canbaeck B., Eriksson A.-S., Nasslund A.K., Handley S.A., Huvet M.,

La Scola B., Holmberg M., Andersson S.G.E.;

"The louse-borne human pathogen Bartonella quintana is a genomic

derivative of the zononcic agent Bartonella henselae.";

Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).

EMBL; BX897699; CAF26991.1; -; Genomic_DNA.

GO; GO:0003824; F:catalytic activity; IEA.
                                                                                                                                                                            EALAARAAL I ESAEHSLDLQYY I WRND I SGRLL FNLMYLAAERGVRVRLLLDDNNTRGLD
                                                                                                                                                                                                                        144 DLLLALDSHPNIEVRLFNPFVLRKW---RALGYLTDFPRLNRRMHNKSFTADNRATILGG
                                                                                                                                                       Gaps
                                                                                                                                                       38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bartonellaceae; Bartonella.
                                                                                                                               Length 523;
                                                                                                                             ; Score 828; DB 2; Length 52; Pred. No. 6.7e-50; 64; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HNRLOWHDPATRKTY - - PNEPEAKLWKRIAAKILSLLPIEGLL 525
Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).
BMBL; BX897700; CAR25571.1; -; Genomic DNA.
GO: 0003434; F: catalytic activity; TEA.
GO; GO: 0003152; P: metabolism; IEA.
InterPro; IPRO01736; PLD.
Fam; PPO0641; PLDO; 2.
SMART; SM00155; PLDC; 2.
SMART; SM00155; PLDC; 2.
COMPLEE PSC6035; PLDC; 2.
COMPLEE PSC6035; PLDC; 2.
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Phopholipase d-family procein.
OrderedLocusNames=BH01790;
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                                                                                                                              30.4%;
                                                                                                                                         Best Local Similarity 43.2*
Matches 200; Conservative
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QGG4X0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 PAYMALDKHPHIEVRMFNPGRSRKGGVRRGLEIILRAITVTRRMHNKAFIVDGRMAFVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 EALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNTRGLD
                                                                                                                                                                                                                                                                                                                                                                             144 DLLLALDSHPNIEVRLFNPFVLRKW---RALGYLTDFPRLNRRMHNKSFTADNRATILGG
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                                                                                                                                                                                                                            30;
                                                                                                                                                                             Length 523;
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Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                     30.3%; Score 825; DB 2; Length 52 41.6%; Pred. No. 1.1e-49; tive 73; Mismatches 165; Indels
                                                                                                                         262FCDC8C269D5AD CRC64;
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Last annotation update)
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DNA Res. 7.31-38 (2000).
EMBL; APO03017; BAB54862.1; -; Genomic DNA.
GO; GO:0003824; F:catalytic activity; ĪEA.
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MEDLINE=21082930; Pubmed=11214968;
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                                                                                                                         523 AA; 59379 MW;
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Q98N23;
01-OCT-2001 (TEMBLFel. 18,
01-OCT-2003 (TEMBLFel. 25,
                                                                                                                                                                                               Best Local Similarity 41.6%;
Matches 191; Conservative 7
InterPro; IPR001736; PLD. Pfam; PF00614; PLDc; 2. SMART; SM0155; PLDc; 2. PROSITE; PS50035; PLD; 2.
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294:2317-2323 (2001)
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SEQUENCE 518 AA
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ID Q984E
AC Q984E
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(BUEX3 QCCUT;

(BUEX3 COCCUT;

(BUEX3 COCCUT;

(BUEX3 COCCUT;

(BUEN2002 (TrEMBLrel. 21, Last sequence update)

11-JUN-2002 (TrEMBLrel. 21, Last sequence update)

13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

Phospholipase D family protein (Agg. C_3007p).

Agrobacterium tumefaciens (strain C58 / ATCC 33970).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

Rhizobiaceae; Agrobacterium.
                                                                                                                                                                                                                                                                                  Query Match

29.9%; Score 812.5; DB 2; Length
Best Local Similarity 42.0%; Pred. No. 7.1e-49;
Matches 197; Conservative 63; Mismatches 176; Indels
                                                                                                        SWART; SW00155; PLDc; 2.
PROSITE; PS50035; PLD; 2.
Complete protecome: Plasmid.
SEQUENCE 466 AA; 51793 MW; 4693C68F20F94F3F CRC64;
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001736; PLD.
Pfam; PF00614; PLDc; 2.
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NOULEGOIDE SEQUENCE.

NUCLEGOIDE SEQUENCE.

NAMBDLIABE-21608551; PubMed=11743194; DOI=10.1126/science.1066803;

A Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,

A Would B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

Houmiel K., Gordon J., Vaudin M., Iartchuk O., Epp A., Liu F.,

Houmiel C., Alinger M., Doughty D., Scott C., Lappas C., Markelz B.,

Randam C., Alinger S.;

A Cielo C., Slater S.;

A Grenome sequence of the plant pathogen and biotechnology agent

Agrobacterium tumefaciens CS8.";

Agrobacterium tumefaciens CS8.";

REMBL, AE009120; AAL42632.1; -; Genomic_DNA.

EMBL, AE009120; AAL42632.1; -; Genomic_DNA.

RABL; AB2777; AB2777;

RABC, GO:0003824; F:catalytic activity; IEA.

RO; GO:0003824; F:catalytic activity; IEA.

RO; GO:0003824; F:catalytic activity; IEA.

RAPCATIC: PRO01136; PLDC; 2.

SMART; SMO0155; PLDC; 2.

RAPCATIC: PSS0035; PLDC; 2.
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Last sequence update)
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098483;
01-OCT-2001 (TrEMBLrel. 16
01-OCT-2001 (TrEMBLrel. 18
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Matches 204; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AYRVTLDKHNRLQWH--DPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 466;
                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          466 AA; 52117 MW; 693301E508A0A788 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Cardiolipin synthetase family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 804.5; DB 2;
Pred. No. 2.6e-48;
1; Mismatches 180;
                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 7:331-338(2000).

EMBL, BA000012; BABB3717.1; -; Genomic DNA. GO; 00003824; F:catalytic activity; TEA. GO; GO:0008152; P:metabolism; IEA. InterPro; IPR001736; PLD. Ffan. PF00614; PLDc; 2. Ffan. PF00614; PLDc; 2. PRN01155; PLDc; 2. PROSITE; PS50035; PLD; 2.
                                                                       Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                          MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.6%;
                                               OrderedLocusNames=mlr8077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 466 AA;
                                                                                                                                         NCBI_TaxID=381;
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Q6FB53 ACIAD
ID Q6FB53 AC
AC Q6FB53;
DT 05-UUL-20
DT 05-UUL-20
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Created)
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(TrEMBLrel. 27, (TrEMBLrel. 27, 1

OFFB53 OFFB53 05-7UL-2004 (TYEMBLYEL) 27, 05-JUL-2004 (TYEMBLYEL) 27, 05-JUL-2004 (TYEMBLYEL) 27,

PRT;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWYEKMTGRVIPA-----KGKKSSSLHAKFFDVDGK-VFIGSFNFDPRSAYLNTEVGLV 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 IESPKIAEQMERTLADITPEYAYRVTLDKHNRLQWHD-PATRKT--YPNEPEAKLWKRIA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 KORYSVKW--AKAHFVADSPKKIHGHAIGNELİYNQMFSIMGHPOKHLELVSAYFVPTQA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 MHNKLIIADNTIAVTGGRNISSEYFDASYQFQFTDLDİLFYGTAASQAEKVFQTFWDSPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 HTPHN--NGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AERGVRVRLLLLDDNNTRGLDDLLLALDSHPNI EVRLFNPFVLRKWRALGYLTDFPRLNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHNKSFTADNRATILGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 AHNATRIIRSGNIGKGLQALGYNDETSRHALLRYRETVEQ--SPLYQKIQTGRID----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVTTQKLITKGQPNDLLQLRS-------KYKE-IERVDTPTEDKINEAQIELNEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----WQSVQTRLISDTPAKGLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVV
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                                                                                                                                                                                                                                              Barbe V., Vallene D., Fonknechten N., Kreimeyer A., Oztas S., Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P., ornston L.N., Weisenbach J., Marliere P., Cohen G.N., Meddigue C.; orningue features revealed by the genome sequence of Anietobacter sp. ADP1, a versatile and naturally transformation competent bacterium." Nucleic Acids Res. 32:5766-5779(2004).

GO: 0016740; Fitransferase activity; IEA.

GO: 0016740; Fitransferase activity; IEA.

Interpro; IPR001735; Pub.

Pfam; PF00614; PLDC; 2.
              Acinetobacter sp. (strain ADP1).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Moraxellaceae, Acinetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.2%; Score 794; DB 2; Length 52 Best Local Similarity 37.7%; Pred. No. 1.7e-47; Matches 186; Conservative 76; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               520 AA; 60385 MW; 1DD312966EA749A0 CRC64;
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Last sequence update)
                                                                                                                                                                                                                       PubMed=15514110; DOI=10.1093/nar/gkh910;
OrderedLocusNames=ACIAD1881
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Q9HTP4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50035; PLD; 2.
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MKAVSYLPIEWMM
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SEOUENCE 520 AA:
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ID Q9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59
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STRAINSATCC 15692 / PAO1;
MEDLINE-2043737; Pubmed=10984043; DOI=10.1038/35023079;
SCOVER C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 RSLISLLCLLLCSCSSWLPP------LEERTESRHFNTSKPVLLDNILQIRHTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRFLLLALLALLACCASTPPPQPSSALPAEGTWLARQAE-------IQGRDHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 HNNGLSDIYLLDDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 RPIEDFLWRAPYPGEL-----ESARRKLQRYLRKESVKESGYIRHLFDRGDQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSGTDALAKLVQDGIDVTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70;
                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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36.7%; Pred. No. 2.4e-47;
ive 86; Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteome, Hypothetical protein.
529 AA; 59199 MW; DABFSED5881E63DE CRC64;
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO, GO:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO:0008654; P:phospholipid biosynthesis; IEA.
InterPro; IPR001736; PLD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 406:959-964(2000).
EMBL; AE004943; AAG08695.1; -; Genomic_DNA
                                                                                                                                                                      Pseudomonadaceae; Pseudomonas
(TrEMBLrel. 26,
                             Hypothetical protein.
OrderedLocusNames=PA5310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             opportunistic pathogen.";
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Matches 200; Conservative
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PROSITE; PS50035; PLD; 2.
                                                                                                       Pseudomonas aeruginosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; F82983; F82983.
                                                                                                                                                                                                                  NCBI_TaxID=287;
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SEQUENCE
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203 AIVGGRNLGDEYFNASPTLOFRDLDVLAAGPVTRAVSASFDAYWSSALTYPLPALNRRY 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305 ISDTPAK-GLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGID 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIVITHSLQAIDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGS-SVTSL 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 RALVLCAALALSGCATHPPATTLERTVSHALPPDASTPLADALAVQARAH-PGESGFVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 DDPHEALAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAAERGVRVRLLLDDNNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 RSLISLLCLLLCSCSSWLPPLE-ERTESRHFNTSKPVLLDNILQIRHTPHNNGLSDIYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E., Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson I Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F., Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yi Satructural flexibility in the Burkholderia mallei genome."; Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.5%; Score 774; DB 2; Length 55 36.1%; Pred. No. 4.8e-46; ative 81; Mismatches 216; Indels
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                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative phospholipase D.
OrderedLocusNames=BMAA0208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 23344;
PubMed=15377793; DOI=10.1073/pnas.0403306101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001736; PLD.
Ffan; PF00614; PLDC; 2.
SMART; SM00155; PLDC; 2.
PROSITE; PS50035; PLD; 2.
                                                                                                                                                                                                                                                                                                                                                                                               Burkholderia mallei (Pseudomonas mallei)
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                                                                                                                                                                         Q62E43 BURMA PRELIMINARY;
Q62E43;
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525 LEKML 529
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SEQUENCE 550 AA
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415 TKAIVFDRRKTFIGSFNFDPRSVLWNTEVGVLVDSPELAE-YTRELAQQGMAPALSYQVK 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTVLTNSLQATDVAAVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLH
                                                                                                                                                     AKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLAD--TTPEYAYRVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=HI2424;
US DOE Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome assembly of Burkholderia cenocepacia HI2424.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Larimer F., Land M., **Annotation of the draft genome assembly of Burkholderia cenocepacia H12444.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORFNāmes=Bccn2424DRAFT 1235;
Burkholderia cenocepacia H12424.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                    LDKHNRLOW--HDPATRKTYPNEPEAKLWKRIAAKILSLLPIEGLL 525
                                                                                                                                                                                                                                                                                                                                                   208; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Phospholipase D/Transphosphatidylase precursor.
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US DOE Joint Genome Institute (JGI-ORNL);
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540 AA; 59105 MW;
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36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q4LJD9_9BURK PRELIMINARY;
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Best Local Similarity 36.8°
Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 PDANDLRASRQRLEVS---LAKAR--TQRKALYDRLMAYQSQPRLDVWRNELIWAHAQAL 294
                      ||| :::| | : || || || || || || || || Hakayudranevanledevtkptisyrut
                                                                                             ---RLOWHDPATR--KTYPNEPEAKLWKRIAAKILSLLPIEGLL
                                                                                                                           HAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTT-PEYAYRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-2242366; Pubmed=12534463; MEDLINE-2242366; Pubmed=12534463; DoI=10.1046/1.1462-2920.2002.00366 x; Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F., Madugu R., Nelson W.C., White O., Peterson J.D., Khouri H.M., Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K., Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 RSLISLICLLL--CSCSSWLPPLEERTESRHFNTSKPVLLDNILQIRHTPHNNGLSDIYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDGLDTVMGTLDAHPNIHIRVFNPLHLGRSTGVTRAVGRLFNLSRQHRRMHNKLFLVDNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas putida (strain KT2440).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
NCBI_TaxID=160488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83; Mismatches 210; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  517 AA; 57574 MW; 107E07900AA35751 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metabolically versatile Pseudomonás putida KT2440.";
Environ. Microbiol. 4:799-808(2002).
EMBL; AE016793; AAN70841.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Phospholipase D family_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008654; P:phospholipid biosynthesis; IEA.
Interpro; IPR001736; PLD.
Pfam; PF00614; PLDc; 2.
                                                                                                                                                                                                                                                                    517
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                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                             Q88CAS_PSEPK PRELIMINARY;
Q88CAS;
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PROSITE; PS50035; PLD; 2
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NUCLEOTIDE SEQUENCE.
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Matches 199;
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---- QSPLYQKIQTGRID--WQSVQT 302
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Worldwine accessions:

Worldwine accessions:

Whender 1537794; DOI=10.1073/pnas.0403302101;

Budder 1537794; DOI=10.1073/pnas.0403302101;

Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,

Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,

Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,

Benchey K., Brown K.A., Brown N.R., Davis P., Deshazer D.,

Chillingworth T., Cronin A., Crossett B., Davis P., Deshazer D.,

Reith K.E., Maddison M., Moule S., Price C., Quail M.A.,

Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,

Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,

Mitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;

Genomic plasticity of the causative agent of melicidosis,

Burkholderia pseudomallei.";

Burkholderia pseudomallei.";

Burkholderia pseudomallei.";

Burkholderia pseudomallei.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
4 pypothetical protein.
OrderedLocushames=BPSS1883;
Burkholderia pseudomallei (Pseudomonas pseudomallei).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales,
Burkholderiaceae, Burkholderia, pseudomallei group.
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SEQUENCE 550 AA; 59557 MW; F12C9179EC17626B CRC64;
                                                              GNIG-KGLOALGYNDETSRHALLRYRETVE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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(TrEMBLrel. 28, I
(TrEMBLrel. 28, I
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Best Local Similarity 35.9%;
Matches 194; Conservative 81
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                                                                                                                                                                                    RGLDDLLLALDSHPNIEVRLFNPFVLRKW----RALGYLTDFPRLNRRMHNKSFTADNRA 195
                                                                                                                                                                                                                              256 IGKGLQALGYNDETSRHALLRY-----RETVEQSPLYQKIQTGRID--WQSVQTRL
                                                                                                                                                                        305 ISDTPAK-GLDRDRRKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGID
                                                                                                                                                                                                                                                              HAKTFIVDGKRIFIGSFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTT-PEYAYRVT
                                                                                                                                                                                                                                                                                                           -----RLQWHDPATR--KTYPNEPEAKLWKRIAAKILSLLPIEGLL
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